

STIC-Biotech/ChemLib

71742

From: Mehta, Ashwin  
Sent: Wednesday, July 24, 2002 2:49 PM  
T : STIC-Biotech/ChemLib  
Subject: seq search

STIC,

Please search the commercial and interference databases for the amino acid seq of SEQ ID NO: 1 and the nucleotide sequence of SEq ID NO: 2 from 09/971,020.

My mail room is 9E12, office 9E07, art unit 1638.

Thank you,  
Ashwin

Ashwin Mehta  
United States Patent and Trademark Office  
Biotechnology Patent Examiner  
703-306-4540

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 7/25/02  
Date Completed: 7/28/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 09  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2002, 03:27:24 ; Search time 242.08 Seconds

(without alignments)  
9205.861 Million cell updates/sec

Title: US-09-971-020-2

Sequence: 1 agcagtcgcaatcgatgtg.....atataaaaaaaaaaaaaa 1298

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq. 032802:\*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138.8	10.7	1427	22	AAC82742
2	138.8	10.7	1427	22	AAC82743
3	134.8	10.4	1363	22	AAF80136
4	129.8	10.0	1407	21	AAC35921
5	126.8	9.8	1239	21	AAC45306
6	90.4	7.0	1170	24	ABA05043
7	90.4	7.0	1345	21	AAC30544
8	90.4	7.0	1476	24	ABA05044
9	50.4	3.9	1206	21	AAC46773

10	48.8	3.8	1211	21	AAC33567	Arabidopsis thaliana
11	43.8	3.4	128	22	AA07727	Cervical cancer pr
12	42.6	3.3	1259	21	AAC48777	Arabidopsis thaliana
13	42.6	3.3	1261	21	AAC36551	Arabidopsis thaliana
14	41.4	3.2	3637	20	AAK60802	Human secreted pro
15	41.4	3.2	3637	22	AAK59208	Human secreted pro
16	41.4	3.2	3637	24	ABA90877	Human cDNA encodin
17	41.2	3.2	5928	24	ABA40877	Human polynucleoti
18	41.2	3.2	5928	24	ABA40877	Human immune syste
19	41	3.2	873	18	AAAD22204	Renilla reniformis
20	41	3.2	1299	18	AAAT73692	DNA encoding aspar
21	41	3.2	1299	19	AAV44040	S. aureus asparagi
22	41	3.2	14041	22	AAH40024	Internal control B
23	40.8	3.1	5294	22	AAH33071	Human immune syste
24	40.6	3.1	612	22	AAH71471	Cervical cancer pr
25	40.6	3.1	612	22	AAH71471	Human cervical can
26	40.6	3.1	623	21	AAC33628	Arabidopsis thaliana
27	40.6	3.1	711	22	AAAL5484	Human breast cance
28	40.6	3.1	5884	24	ABL34164	Human immune syste
29	40.6	3.1	15247	24	ABL34083	Human immune syste
30	40.4	3.1	425	22	AAK60450	Human cancer agent
31	39.8	3.1	664	21	AAK26336	Human secreted pro
32	39.8	3.1	3839	21	AAAD01314	Human immune syste
33	39.8	3.1	6365	24	ABL32124	Human immune syste
34	39.8	3.1	9965	24	ABL33527	Human immune syste
35	39.6	3.1	56153	22	AAK46793	Tumour suppressor
36	39.6	3.1	6185	22	ABL32413	Human immune syste
37	39.6	3.1	19734	24	ABA83286	Human immune syste
38	39.4	3.0	1830	20	AAK00612	Human secreted pro
39	39.4	3.0	1830	21	AAK98100	Human secreted pro
40	39.4	3.0	1830	22	AAAD1713	Human secreted pro
41	39.4	3.0	1842	21	AAK98096	Human secreted pro
42	39.4	3.0	1842	22	AAAD1709	Human secreted pro
43	39.4	3.0	2218	20	AAV84503	Human secreted pro
44	39.4	3.0	2218	22	ABA83415	Human secreted pro
45	39.4	3.0	6311	24	ABL33963	Human immune syste

## ALIGNMENTS

RESULT 1	
AC82742	standard; DNA; 1427 bp.
AC82742	
16-MAR-2001 (first entry)	
C. sinensis N-methyl transferase DNA	
Caffeine biosynthesis; N-methyl transferase; tea; N-met; plant; ds.	
Camellia sinensis	
EP1055727-A2	
29-NOV-2000.	
26-MAR-2000; 2000EP-0304522.	
26-MAR-1999; 99UP-0146358.	
(MITA) MITSUI CHEM INC.	
Mizuno M, Ashihara H, Mizuno K, Fujimura T,	
WPI: 2001-063619/08.	
P-PSDB: AAB45799.	
DNA encoding N-methyl transferase with enzyme activities of 7-methyl	
xanthine N3 methyl transferase, theobromine N1 methyl transferase and	
paraxanthine N3 methyl transferase, useful for caffeine synthesis in	



QY 94 tgcattcactacatctgctcttgc--caaggltgaaaccttcttctgaacaatgcataca 151  
 DB 140 cttctctctctctctctctctctctctctctctctctctctctctctctctctctct 199  
 QY 152 gaattgttgcggcgcaactctgccaacatcaacaagttgccaagtctggaattgga 211  
 DB 200 aacucucucucacagagauuucc-----accuacagcucuaacagcgagcgagcuu 254  
 QY 212 tgccttctgaccacaacacatttaacgtgcggagacattgtgcaaaatgatacaaa 271  
 DB 255 ugugcagcgagcagcaacacacacacacacacacacacacacacacacacacacac 314  
 QY 272 gtgcgcaaggaagaagaagaatagaaagtcgccaacacacacacacacacacacacac 331  
 DB 315 aauagcaggaauaga-----aauagcaggaagcagcagcagcagcagcagcagcagc 368  
 QY 332 cttctcacaacacacacacacacacacacacacacacacacacacacacacacacac 391  
 DB 369 cuuuuugagaauuacacacacacacacacacacacacacacacacacacacacacacac 416  
 QY 392 gagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 451  
 DB 417 guuuuugagaauuacacacacacacacacacacacacacacacacacacacacacacac 476  
 QY 452 tgcgcaacacacacacacacacacacacacacacacacacacacacacacacacacac 511  
 DB 477 caugcgcgcuuuuucucuaacacacacacacacacacacacacacacacacacacacacac 536  
 QY 512 tgcattcactacagttcccgagcggttggtgattggaattggaattggaattggaattg 571  
 DB 537 ugugcagcgagcagcaacacacacacacacacacacacacacacacacacacacacacac 596  
 QY 572 agtatttactctcacaagaagatgtctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 631  
 DB 597 aagaauuacacacacacacacacacacacacacacacacacacacacacacacacacac 656  
 QY 632 acgaaagatttccacacacacacacacacacacacacacacacacacacacacacacac 691  
 DB 657 caugagaauuacacacacacacacacacacacacacacacacacacacacacacacacac 716  
 QY 692 atgctctcactctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 739  
 DB 717 augguugagaauuacacacacacacacacacacacacacacacacacacacacacacacac 776  
 QY 740 ccccaagacacacacacacacacacacacacacacacacacacacacacacacacacac 799  
 DB 777 acuuugagaauuacacacacacacacacacacacacacacacacacacacacacacacac 836  
 QY 800 gaaatattgattgattcattcattcattcattcattcattcattcattcattcattcatt 859  
 DB 837 gaaatattgattgattcattcattcattcattcattcattcattcattcattcattcatt 896  
 QY 860 atagttgaggaagaaggtctctgcgaatttatactcgtgagaacttta 909  
 DB 897 aauagcaggaagcagcauucacacacacacacacacacacacacacacacacacacacac 946  
 RESULT 3  
 ID AAF80136 standard; DNA; 1363 BP.  
 AC AAF80136;  
 XX 11-JUN-2001 (first entry)  
 DE Snapdragon benzoic acid carboxyl methyltransferase (BAMT) DNA.  
 XX Snapdragon: benzoic acid carboxyl methyltransferase; BAMT; floral scent;  
 KW S-adenosyl-L-methionine:benzoic acid carboxyl methyltransferase;  
 methyl benzoate; transgenic plant; ss.  
 OS Antirrhinum majus.

XX Key Location/Qualifiers  
 FH CDS 19..113  
 FT /tag= a  
 FT /product= "benzoic acid carboxyl methyltransferase"  
 WO200118183-A1.  
 XX 15-MAR-2001.  
 XX 01-SEP-2000; 2000WO-US24362.  
 XX 03-SEP-1999; 99US-0152393.  
 XX (PURD ) PURDUE RES FOUND.  
 XX Doudareva N, Murfitt LM, Mann CJ;  
 DR MPT: 2001-244568/25.  
 DR P-PSDB; AAB67769.  
 XX Novel purified benzoic acid carboxyl methyltransferase protein useful  
 PT for production of floral scent compounds and biosynthesis  
 XX Claim 9; Page 85-88; 94pp; English.  
 XX The present sequence encodes a Snapdragon benzoic acid carboxyl  
 CC methyltransferase (BAMT) protein. The protein is a  
 CC S-adenosyl-L-methionine:benzoic acid carboxyl methyltransferase, and  
 CC the enzyme is used in the formation of floral scent compounds such as  
 CC methyl benzoate. The enzyme catalyzes the transfer of a methyl group  
 CC donor, such as S-adenosyl methionine (SAM) to benzoic acid to form  
 CC methyl benzoate. BAMT proteins are useful for the production of floral  
 CC scent compounds and biosynthesis. BAMT polynucleotides are useful for  
 CC producing transgenic plants.  
 SO Sequence 1363 BP; 417 A; 239 C; 300 G; 407 T; 0 other;  
 Query Match 10.4%; Score 134.8; DB 22; Length 1363;  
 Best Local Similarity 49.6%; Pred. No. 3.4e-26;  
 Matches 546; Conservative 0; Mismatches 482; Indels 72; Gaps 5;  
 QY 59 aatgaggtgtaagcgatcacatgaacgacgaagaatgatctacacacacacacacacacac 118  
 DB 52 atgcaagagatggtgtaaacatgactacgacacacacacacacacacacacacacacacac 111  
 QY 119 aagtggaacacacacacacacacacacacacacacacacacacacacacacacacacac 178  
 DB 112 tcaaacacacacacacacacacacacacacacacacacacacacacacacacacacacac 171  
 QY 179 atcaacacacacacacacacacacacacacacacacacacacacacacacacacacacac 238  
 DB 172 tcccaaacacacacacacacacacacacacacacacacacacacacacacacacacacacac 231  
 QY 239 acagtgcggaacacacacacacacacacacacacacacacacacacacacacacacacac 298  
 DB 232 gcaacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 288  
 QY 299 gaagtcacacacacacacacacacacacacacacacacacacacacacacacacacacacac 358  
 DB 289 gaattacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 348  
 QY 359 ttcaacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 418  
 DB 349 ttcaacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 375  
 QY 419 tctgctcactaagcgaatgctgctctctcactacacacacacacacacacacacacacacacac 478  
 DB 376 aactctcttataatgattgttcgctcctctctcaggaacacacacacacacacacacacacac 435  
 QY 479 atgcatcttctgacacacacacacacacacacacacacacacacacacacacacacacacacac 538



Db 436 ctacacttgcttattctctctacagatctacatctcgtctctcgtctctcgtcgaaggtcgt 495  
OY 539 gtgattgaattgggattgtgtgcacaagaaggagattacttactctccaaagatgctgt 598  
Db 496 gagataat-----aacagcaaaacatttaccagtaagcaaggaagctct 540  
OY 599 ccgcccgcacgaagcatatttgatcatttaagaagatttaccacatttaagg 658  
Db 541 ccgaagtgacaaagcatcagcaagcaatacgaagaagagcttcccaatttcaag 600  
OY 659 attcattcgaagaagttgttctcagcggcgaagccttaccgcttcttgaagta 718  
Db 601 ttggcagcggaggaatgtgtaccgcgtgagcgcagtgcttgaacttaagcagaagt 660  
OY 719 gatga-----ttgcacgaacgcgaatccctagacttacttaccatgagcaata 766  
Db 661 gtgcagaatccctgcagcaagaagatgacttagcaatttccatctgtgcacaaacacta 720  
OY 767 aacgaacttgattgtgaggaactcttgaggaagaataatgatagtttccataatcca 826  
Db 721 gtgatatgtgtgctgagggctgtgcaagatgagcgaattgttactcgtttacattcct 780  
OY 827 tctcttaccctcagcagaagaagtaagtgacatagttgagaggaaggtcttcgcga 886  
Db 781 attaccacaccatgtagcgcgaagtagagcaaatcttgaagtgaggtcttctttag 840  
OY 887 atttatactgagacatttaaggccattatgtctgtcctctctatgatgat 946  
Db 841 ttggcagcgttagaggtcttctgtgtgtgtgagtgatgacatgctacacagatgacat 900  
OY 947 -----faccagtaagatcccatgacaataatgaagaaggtgttgcacatta 997  
Db 901 gatcagaagaacccatcatcttggcaacaagaagagtgaaatcttggcagaatcgt 960  
OY 998 attgacatgattgaacatccatctcgcgaagtcatttggagaagctattatgcctgac 1057  
Db 961 gtaaggcctcttgcgaacaaatgctgtcgaacatttggagacatactatggatcct 1020  
OY 1058 ttattcacaaggtctgcgaagcatgacgaagaaggtctccacatggcgaaggtcgtat 1117  
Db 1021 ctatttggaaagatgacaaagaataagtgagacatctatcgtggagaacttcgcatat 1080  
OY 1118 ataactcttactctct 1137  
Db 1081 ttacagcatagtagttctct 1100

RESULT 4  
AAC35921  
ID AAC35921 standard; DNA: 1407 BP.  
XX  
AC AAC35921;  
XX  
DT 17-OCR-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 11896.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132853.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135659.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137558.  
PR 04-JUN-1999; 99US-0137552.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139783.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143634.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.

PR	08-OCT-1999;	9905-01582322.
PR	12-OCT-1999;	9905-0158369.
PR	13-OCT-1999;	9905-01592923.
PR	13-OCT-1999;	9905-01592924.
PR	13-OCT-1999;	9905-01592925.
PR	14-OCT-1999;	9905-01593329.
PR	14-OCT-1999;	9905-01593330.
PR	14-OCT-1999;	9905-01593331.
PR	14-OCT-1999;	9905-01596337.
PR	14-OCT-1999;	9905-01596368.
PR	18-OCT-1999;	9905-01595684.
PR	21-OCT-1999;	9905-01607241.
PR	21-OCT-1999;	9905-0160767.
PR	21-OCT-1999;	9905-01607768.
PR	21-OCT-1999;	9905-01607770.
PR	21-OCT-1999;	9905-0160814.
PR	21-OCT-1999;	9905-0160815.
PR	22-OCT-1999;	9905-0160980.
PR	22-OCT-1999;	9905-0160981.
PR	22-OCT-1999;	9905-0160989.
PR	25-OCT-1999;	9905-0161404.
PR	25-OCT-1999;	9905-0161405.
PR	25-OCT-1999;	9905-0161406.
PR	25-OCT-1999;	9905-0161359.
PR	26-OCT-1999;	9905-0161360.
PR	26-OCT-1999;	9905-0161361.
PR	28-OCT-1999;	9905-0161920.
PR	28-OCT-1999;	9905-0161992.
PR	28-OCT-1999;	9905-0161993.
PR	28-OCT-1999;	9905-0162142.

```
Db 701 aagtcacatacaagcctactgaatcaatccaaaagacttaccatggttcaaggt 760
Qy 661 tcaatcgaaagatgcttcttcacgtgcgaatgctccttaccatctgttaagtaga 720
Db 761 acgttctgaagaatgctctcctcaatgacgtatgcttccacttccggaagaacac 820
Qy 721 tgaattcgacgaacccatcccttagact-----tacttgacatgcaataaa----- 768
Db 821 tcttaacgacatccttctatagagatggtgtcctacttcttgacatgcatcaactctc 880
Qy 769 ---cgaattgcttgagagactcttgagagaaagaataatgcttgaattcattctcc 825
Db 881 ccgttgcactagctcttctgaggtcttgagtgagtaagtcgaagcgtcgcattcaacatg 940
Qy 826 attcttcaccccttcagcagaagaagtaagtgacaaagtggaggaagttcttcgga 885
Db 941 gtttaatgacacgaagtcacgaactcaagaagtgatacaaaaagagcctcttga 1000
Qy 886 aatttatacttgagactttaagccacttattgtgtcttctctctatgataga 945
Db 1001 aatcaatgaattgag---tcaatgatttgatcttgacactacacgaagaagataga 1057
Qy 946 taccacgaatgaatccatgacgaacaaatgaagaagtatgtgcatacttaatgac 1005
Db 1058 ctctgaagaagacgaacgaacga-----gctaattgacataagac 1096
Qy 1006 agttaacgaacccatccctgcgaagctatttgagaagctattatgcattatcca 1065
Db 1097 tgtttagtgaaccaatgctcatctgctcatttggagaagaatatacctctgttga 1156
Qy 1066 caggtcttcgaagaatgacgaagaagttctccacagggcagaagctgcataatatc 1125
Db 1157 taagatgcatcacatgctgacccaacacagccaactcagaagaacaaagcctgcact 1216
Qy 1126 tatcatctctctcccaaaaagccagagaagtcagacgt 1166
Db 1217 tgtcttctcttgactgaagaagtaacactctgcacgt 1257

RESULT 5
AAC45306 standard; DNM; 1239 BP.
ID AAC45306;
AC AAC45306;
AT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46034.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 03-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0135629.
PR 26-MAY-1999; 99US-0135629.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139464.
PR 18-JUN-1999; 99US-0139465.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
```

PR 20-JUL-1999; 99US-0144632.  
 PR 20-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0144814.  
 PR 21-JUL-1999; 99US-0145086.  
 PR 21-JUL-1999; 99US-0145088.  
 PR 22-JUL-1999; 99US-0145085.  
 PR 22-JUL-1999; 99US-0145087.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 22-JUL-1999; 99US-0145192.  
 PR 23-JUL-1999; 99US-0145145.  
 PR 23-JUL-1999; 99US-0145218.  
 PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145913.  
 PR 27-JUL-1999; 99US-0145918.  
 PR 27-JUL-1999; 99US-0145951.  
 PR 28-JUL-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 03-AUG-1999; 99US-0146389.  
 PR 04-AUG-1999; 99US-0147038.  
 PR 04-AUG-1999; 99US-0147302.  
 PR 05-AUG-1999; 99US-0147192.  
 PR 06-AUG-1999; 99US-0147260.  
 PR 06-AUG-1999; 99US-0147303.  
 PR 09-AUG-1999; 99US-0147416.  
 PR 09-AUG-1999; 99US-0147493.  
 PR 10-AUG-1999; 99US-0147935.  
 PR 11-AUG-1999; 99US-0148171.  
 PR 12-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148565.  
 PR 13-AUG-1999; 99US-0148584.  
 PR 15-AUG-1999; 99US-0149364.  
 PR 15-AUG-1999; 99US-0149375.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-0151338.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 23-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158332.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.

PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 21-OCT-1999; 99US-0160880.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160982.  
 PR 22-OCT-1999; 99US-0161402.  
 PR 22-OCT-1999; 99US-0161404.  
 PR 22-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161820.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 9.8%; Score 126.8; DB 21; Length 1239;  
 Best Local Similarity 51.0%; Pred. No. 4,7e-24;  
 Matches 562; Conservative 0; Mismatches 462; Indels 78; Gaps 8;

OY 61 tgaagtgaaagcgatcaagcgatcagcgaagaatgcatccctcaaatctgctctgcaaa 120  
 DB 200 tgaagtgatgctcgaacagcttaccgctcgcgaattcgccttcagaaagaattatcaat 259  
 OY 121 ggtgaacaccttccttgaaacagtgatcaggaattgtgcggccaactggccaacat 180  
 DB 260 ggcacaacacagctctgttaagaacacaggaagaatgatgatgaac-----ttaacct 313  
 OY 181 caacaaagcgatcgaatgaatgctggaattggaatgctgctggaacacacacactttaac 240  
 DB 314 tcttaagatcaacaaatgctgaattggtgtcttcgcgcaaaactcttttggg 373  
 OY 241 agtcgagacattgtcaaaagtgtgacaagtgtgcgaggaagaagaatgatataga 300  
 DB 374 taacttgcgatacacaacacacatgaatgtgtgtgcgaacagtggaacaaacatca-- 431  
 OY 301 acgtccaccactcaagattcttcgaatgaatcctttccaaatgatccaattcgtgttt 360  
 DB 432 ---ccagagatcgattgtgtcttaacgatactccggaaaatgatccaacagacctt 487  
 OY 361 caagtgtcgcgaagcttctacccgaactcgaagaagaagaatgatgacgaatagatc 420  
 DB 488 taagtgcgtacaccttcttcaacaaagagctcatgatcaca-----aacaatcatc 538  
 OY 421 gtgcctaataagcgaaatgctgtgctcttctacgagacactctcccgagagttccat 480  
 DB 539 atgttcgctatagagctccaggtctctctcatcagagctctctctcgcataagacct 598  
 OY 481 gaatttttcgacctgtttacagtggttcattgtgtatcccaagttuccaagcggattggt 540  
 DB 599 ccatttaataacttcccttcatgactccatcattgctcctcaaggtcccggaatctga 658  
 OY 541 gattgatattgggattgtgtgcaacaaaggaatattactcttccaaagagatctgtcc 600  
 DB 659 gaat-----aataagggaatcgtlatatacaaaagttaagtcctca 700  
 OY 601 gccgcgcgaagcgatatttgatataattacgaagaatttccacaactttccaagat 660  
 DB 701 aagttgaatacgaagcctactcgaatcaatccaaagaagcttcaacatgcttcaaggt 760  
 OY 661 tcaattgaagaagtgatttccacggtgcggaatgctcctcaactgcatattgtaagtaga 720  
 DB 761 acgttctgaagaatgtctcttaatgagatgtgtcttcaactctatggaagaacac 820  
 OY 721 tgaattcgacgaacgaatcccttagacttac-----ttgacatggaataaac----- 769

Db 821 tcttaacgacatcgtatagatggttgcaacttttgacatctgacaaactctc 880  
 QY 770 ----gacttattgttgaggactctcgagagaaataattgatttcaatctc 825  
 Db 881 ccgtgacctgacttcttgaggtcttgagatgagcaaggttgacgcttcaaatgc 940  
 QY 826 attcttacccttcagacagagaaatgagatgagatgagagagagagagagag 885  
 Db 941 gttttagatgacagacagacagacagacagacagacagacagacagacagac 1000  
 QY 886 aatttatctgagacatttaagccattatgctgctcctcctcattgagatga 945  
 Db 1001 aatcaatgatttgag-----tcaatgatttgattctgttactactacgaagaatga 1057  
 QY 946 ttaccagtgagatccctcagacaaataaagcagagatgctgacatcttaatagc 1005  
 Db 1058 cttgagagcagagacagatga-----gctatgagcataagagc 1096  
 QY 1006 agtttaagacccatccctcagacatcttcttgagagatctatgctgacttcca 1065  
 Db 1097 tgttagtgaacaaatgctcattcttcttgagagaaatctatgacttcttga 1156  
 QY 1066 caggtctgcaagacagacagagagagagagagagagagagagagagagag 1125  
 Db 1157 taagtagcatcactgactgactcaacatgcaacatgcaagagagagagagag 1216  
 QY 1126 tatcattctctcgcaaaag 1147  
 Db 1217 tgcgttctcctgactaagag 1238  
 RESULT 6  
 ID ABA05043 standard: cDNA: 1170 BP.  
 AC ABA05043:  
 XX  
 DT 22-FEB-2002 (first entry)  
 DE A thaliana jasmonic acid carboxyl methyltransferase coding sequence #1.  
 XX  
 DE Jasmonic acid carboxyl methyltransferase; virus resistance;  
 KM Insect resistance; cold resistance; drought resistance; antifungal;  
 KM S-adenosyl-L-methionine: jasmonic acid carboxyl methyltransferase;  
 KM bacterial phytopathogen resistance; salt resistance; JMT;  
 KM antibacterial; antiviral; transgenic plant; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1170  
 FT /tag="a  
 FT /product="jasmonic acid carboxyl methyltransferase"  
 PN MO200196549-A1.  
 XX  
 PD 20-DEC-2001.  
 XX  
 PF 05-JUN-2001; 2001WO-KR00953.  
 XX  
 PR 13-JUN-2000; 2000KR-0032365.  
 XX  
 PA (SCIG-) SCIGEN HARVEST CO LTD.  
 PA (CHOI/) CHOI Y.  
 PI Choi Y, Cheong J, Lee J, Song J, Song S, Seo H, Koo Y;  
 XX WPI, 2002-090208/12.  
 DR P-Psdb; AAM47309.  
 XX  
 PT Jasmonic acid carboxyl methyltransferase and gene encoding it useful  
 PT for enhancing resistance of plant against damages caused by  
 PT phytopathogens and harmful insects, and stresses

XX  
 PS Claim 3; Page 48-49; 56pp; English.  
 CC  
 CC The present invention relates to the Arabidopsis thaliana jasmonic acid  
 CC carboxyl methyltransferase (JMT, also known as S-adenosyl-L-methionine:  
 CC jasmonic acid carboxyl methyltransferase). The sequences can be used to  
 CC produce transgenic plants with increased resistance to cold, salt,  
 CC drought, viruses, harmful insects and bacterial phytopathogens. The  
 CC present sequence is one version of the cDNA of the invention.  
 XX  
 SO Sequence 1170 BP; 317 A; 244 C; 269 G; 310 T; 0 other;  
 Query Match 7.08; Score 90.4; DB 24; Length 1170;  
 Best Local Similarity 48.48; Pred. No. 2,9e-14;  
 Matches 380; Conservative 0; Mismatches 351; Indels 39; Gaps 4;  
 QY 415 agatgctgcttaataagcgaatgctgctcttctcagagcagacatctcccgagga 474  
 Db 393 agaatgctgcttctgctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 452  
 QY 475 gtcacatgcatcttttgcacctctgttacaggtgattgtatctcaggtcccgagcg 534  
 Db 433 gacgttcacattgtgacatcttctctctatgattggtgtgtcaggttccatgctcg 512  
 QY 535 ttgttgatgattggtggtat-----tggtcaacaagagagatatta 579  
 Db 513 tgagcgagagagagagagagagagagagagagagagagagagagagagagagagag 572  
 QY 580 ctctccaaagagatgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 639  
 Db 573 catatcaagagacagctccttaagatgagatgagatgagatgagatgagatgagatgag 632  
 QY 640 tttaacacattctcaagatcttcttgaagagagagagagagagagagagagagagag 699  
 Db 633 ttcttgcttcttgaagatcttgaagatcttgaagatcttgaagatcttgaagatcttga 692  
 QY 700 taactgacttctt--aaagtatgattctgagaccca-----atccctatga 747  
 Db 693 atgcttcttgaagagagagagagagagagagagagagagagagagagagagagagag 752  
 QY 748 cttaactgacatgacataaagacatgattgttgagagactctgagagagagagagagag 807  
 Db 753 actcctgctcaagctccttaagatgacatgagcagaaagagatctatcagagagagagag 812  
 QY 808 ggaatgattcaatctcattcttcaacatctcagacacagagagagagagagagagagag 867  
 Db 813 cgatgcttcaagctccttactatgctgagctcgcgaagagagagagagagagagagagag 872  
 QY 866 ggaagagagagagagagagagagagagagagagagagagagagagagagagagagag 927  
 Db 873 gaaagagagagagagagagagagagagagagagagagagagagagagagagagagag 932  
 QY 928 ctctctatgattgatttaccagta-----agatccatgagacaaatga 975  
 Db 933 gattatcagagagagagagagagagagagagagagagagagagagagagagagagagag 992  
 QY 976 agcagagatgagagagagagagagagagagagagagagagagagagagagagagagag 1035  
 Db 993 tggcagagagagagagagagagagagagagagagagagagagagagagagagagagag 1052  
 QY 1036 tggagagagagagagagagagagagagagagagagagagagagagagagagagagag 1095  
 Db 1053 cgtgagagagagagagagagagagagagagagagagagagagagagagagagagagag 1112  
 QY 1096 ccacatgagagagagagagagagagagagagagagagagagagagagagagagagagag 1145  
 Db 1113 ctatgaagctgcagacagatagctattgtattcttctgctcgttagaa 1162  
 RESULT 7  
 ID AAC39544 standard: DNA: 1345 BP.

```
XX AAC39544; PR 18-JUN-1999; 99US-0139462.
XX AC PR 18-JUN-1999; 99US-0139463.
XX 17-OCT-2000 (first entry) PR 18-JUN-1999; 99US-0139750.
XX PR 18-JUN-1999; 99US-0139763.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 25021. PR 21-JUN-1999; 99US-0139817.
XX PR 22-JUN-1999; 99US-0139899.
XX PR 23-JUN-1999; 99US-0140353.
XX PR 24-JUN-1999; 99US-0140354.
KW Hybridisation assay; genetic mapping; gene expression control; PR 28-JUN-1999; 99US-0140695.
KW Protein identification; signal transduction pathway; PR 29-JUN-1999; 99US-0140951.
KW Metabolic pathway; promoter; termination sequence; ss. PR 30-JUN-1999; 99US-0141287.
OS PR 01-JUL-1999; 99US-0141542.
XX Arabidopsis thaliana. PR 02-JUL-1999; 99US-0142053.
XX EPI033405-A2. PR 06-JUL-1999; 99US-0142803.
XX PR 08-JUL-1999; 99US-0142820.
XX PR 12-JUL-1999; 99US-0142877.
XX PR 13-JUL-1999; 99US-0143542.
XX PR 14-JUL-1999; 99US-0143624.
XX PR 16-JUL-1999; 99US-0144005.
XX PR 16-JUL-1999; 99US-0144085.
XX PR 16-JUL-1999; 99US-0144086.
XX PR 19-JUL-1999; 99US-0144325.
XX PR 19-JUL-1999; 99US-0144331.
XX PR 19-JUL-1999; 99US-0144332.
XX PR 19-JUL-1999; 99US-0144333.
XX PR 19-JUL-1999; 99US-0144334.
XX PR 19-JUL-1999; 99US-0144335.
XX PR 20-JUL-1999; 99US-0144352.
XX PR 20-JUL-1999; 99US-0144684.
XX PR 21-JUL-1999; 99US-0144814.
XX PR 21-JUL-1999; 99US-0145086.
XX PR 21-JUL-1999; 99US-0145088.
XX PR 22-JUL-1999; 99US-0145085.
XX PR 22-JUL-1999; 99US-0145087.
XX PR 22-JUL-1999; 99US-0145089.
XX PR 22-JUL-1999; 99US-0145192.
XX PR 23-JUL-1999; 99US-0145145.
XX PR 23-JUL-1999; 99US-0145218.
XX PR 26-JUL-1999; 99US-0145274.
XX PR 27-JUL-1999; 99US-0145616.
XX PR 27-JUL-1999; 99US-0145813.
XX PR 27-JUL-1999; 99US-0145818.
XX PR 28-JUL-1999; 99US-0145819.
XX PR 28-JUL-1999; 99US-0145851.
XX PR 02-AUG-1999; 99US-0146386.
XX PR 02-AUG-1999; 99US-0146388.
XX PR 02-AUG-1999; 99US-0146389.
XX PR 03-AUG-1999; 99US-0147038.
XX PR 04-AUG-1999; 99US-0147204.
XX PR 05-AUG-1999; 99US-0147302.
XX PR 05-AUG-1999; 99US-0147192.
XX PR 05-AUG-1999; 99US-0147260.
XX PR 06-AUG-1999; 99US-0147303.
XX PR 06-AUG-1999; 99US-0147416.
XX PR 09-AUG-1999; 99US-0147493.
XX PR 09-AUG-1999; 99US-0147935.
XX PR 10-AUG-1999; 99US-0148171.
XX PR 11-AUG-1999; 99US-0148319.
XX PR 12-AUG-1999; 99US-0148341.
XX PR 13-AUG-1999; 99US-0148651.
XX PR 13-AUG-1999; 99US-0148684.
XX PR 16-AUG-1999; 99US-0149368.
XX PR 17-AUG-1999; 99US-0149378.
XX PR 18-AUG-1999; 99US-0149426.
XX PR 20-AUG-1999; 99US-0149722.
XX PR 20-AUG-1999; 99US-0149723.
XX PR 23-AUG-1999; 99US-0149902.
XX PR 23-AUG-1999; 99US-0149930.
XX PR 18-JUN-1999; 99US-0139462.
XX PR 18-JUN-1999; 99US-0139463.
XX PR 18-JUN-1999; 99US-0139750.
XX PR 18-JUN-1999; 99US-0139763.
XX PR 21-JUN-1999; 99US-0139817.
XX PR 22-JUN-1999; 99US-0139899.
XX PR 23-JUN-1999; 99US-0140353.
XX PR 24-JUN-1999; 99US-0140354.
XX PR 28-JUN-1999; 99US-0140695.
XX PR 29-JUN-1999; 99US-0140951.
XX PR 30-JUN-1999; 99US-0141287.
XX PR 01-JUL-1999; 99US-0141542.
XX PR 02-JUL-1999; 99US-0142053.
XX PR 06-JUL-1999; 99US-0142803.
XX PR 08-JUL-1999; 99US-0142820.
XX PR 12-JUL-1999; 99US-0142877.
XX PR 13-JUL-1999; 99US-0143542.
XX PR 14-JUL-1999; 99US-0143624.
XX PR 16-JUL-1999; 99US-0144005.
XX PR 16-JUL-1999; 99US-0144085.
XX PR 16-JUL-1999; 99US-0144086.
XX PR 19-JUL-1999; 99US-0144325.
XX PR 19-JUL-1999; 99US-0144331.
XX PR 19-JUL-1999; 99US-0144332.
XX PR 19-JUL-1999; 99US-0144333.
XX PR 19-JUL-1999; 99US-0144334.
XX PR 19-JUL-1999; 99US-0144335.
XX PR 20-JUL-1999; 99US-0144352.
XX PR 20-JUL-1999; 99US-0144684.
XX PR 21-JUL-1999; 99US-0144814.
XX PR 21-JUL-1999; 99US-0145086.
XX PR 21-JUL-1999; 99US-0145088.
XX PR 22-JUL-1999; 99US-0145085.
XX PR 22-JUL-1999; 99US-0145087.
XX PR 22-JUL-1999; 99US-0145089.
XX PR 22-JUL-1999; 99US-0145192.
XX PR 23-JUL-1999; 99US-0145145.
XX PR 23-JUL-1999; 99US-0145218.
XX PR 26-JUL-1999; 99US-0145274.
XX PR 27-JUL-1999; 99US-0145616.
XX PR 27-JUL-1999; 99US-0145813.
XX PR 27-JUL-1999; 99US-0145818.
XX PR 28-JUL-1999; 99US-0145819.
XX PR 28-JUL-1999; 99US-0145851.
XX PR 02-AUG-1999; 99US-0146386.
XX PR 02-AUG-1999; 99US-0146388.
XX PR 02-AUG-1999; 99US-0146389.
XX PR 03-AUG-1999; 99US-0147038.
XX PR 04-AUG-1999; 99US-0147204.
XX PR 05-AUG-1999; 99US-0147302.
XX PR 05-AUG-1999; 99US-0147192.
XX PR 05-AUG-1999; 99US-0147260.
XX PR 06-AUG-1999; 99US-0147303.
XX PR 06-AUG-1999; 99US-0147416.
XX PR 09-AUG-1999; 99US-0147493.
XX PR 09-AUG-1999; 99US-0147935.
XX PR 10-AUG-1999; 99US-0148171.
XX PR 11-AUG-1999; 99US-0148319.
XX PR 12-AUG-1999; 99US-0148341.
XX PR 13-AUG-1999; 99US-0148651.
XX PR 13-AUG-1999; 99US-0148684.
XX PR 16-AUG-1999; 99US-0149368.
XX PR 17-AUG-1999; 99US-0149378.
XX PR 18-AUG-1999; 99US-0149426.
XX PR 20-AUG-1999; 99US-0149722.
XX PR 20-AUG-1999; 99US-0149723.
XX PR 23-AUG-1999; 99US-0149902.
XX PR 23-AUG-1999; 99US-0149930.
```

```

PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151085.
PR 27-AUG-1999; 99US-0151086.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158365.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0158294.
PR 13-OCT-1999; 99US-0158295.
PR 14-OCT-1999; 99US-0159325.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161932.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.

```

Query Match 7.0%; Score 90.4; DB 21; Length 1345;

Best Local Similarity 49.4%; Pred. No. 3,1e-14;

Matches 380; Conservative 0; Mismatches 351; Indels 39; Gaps 4;

```

QY 415 agagatgctgcaataaagcaatgctgctcttcaagcagagactcttcccgagga 474
DB 441 agaatcgctgttggtgctgagccaggttcgtctacaggaagttgttcttcgcgcg 500
QY 475 ggcacatgatttttgcacactttgtaagttgattgattacaggttccagcg 534
DB 501 ggccttcacatttgatctctctcttcttaacttgggttgcaggttccatgcgcg 560
QY 535 ttgttgattgaatttgggagat-----tgggtcaacaagaaggagatttta 579
DB 561 tgaagcgaggaagaagaagacagaacaataacagctgatttaagaacaattgggaataata 620
QY 580 ctcttcacaagaagatgctgcgcgcgtccagagaaagcatatttgataatttaagaaga 639
DB 621 cataccaagaagaagctccaagaagtgcacataagaactatgcttccaattccaactga 680

```

```

QY 640 tttaacacatttcaagaatcatctgaagaagttgtttcacgtgagccaaatgctct 639
DB 661 ttctcttgcttttttgaagtaacagatcagtgaggttgcctccggagagccgaatgtttc 740
QY 700 taactgattt--aaagtatgtaattgcagaccca-----atccctaga 747
DB 741 atcttctcttgaagaagatacactggatcccaaacgaaagagtgatgtatacaatgga 800
QY 748 cttaactgataatgaataaagaacttgatttgaaggacttcctggaggaagaanaat 807
DB 801 actcttgatccaagctcttaagtaacagccaagaaggttatcatcgagaagaagaat 860
QY 808 ggaagattcaatattccatcttatacccttcagcaagaagaagtaagtgatgttga 867
DB 861 ggaagaggttcttgcgaattttatatactggaagacttlaagcccatatgagtcgc 927
QY 921 gaagaagaaggttcttgcagatagcgtatgagataagtcgatttgattgggaagtcg 980
QY 928 ctctctatgataatgatttaccagta-----gattccaggaacaataaa 975
DB 981 gagatcagtgagagagatttgaacttgataaagtcacaaccgaagccctagctag 1040
QY 976 agcagagatgagagatcaatcaatcaatgaatgaatgaatgaatgaatgaatgaat 1035
DB 1041 tggcgaagaagtgcttaataacaaagagcttggcgaagcagatgagaaacacatt 1100
QY 1036 tggagaagctatattgctgacttattccacaggttgcgaagatgcagcaaggtct 1095
DB 1101 cggggaanaagtgatgagagacttlttgaagaagtatcaagagcttgcggagaaact 1160
QY 1096 ccaatgaggaaggtctgataataatcttacttctctgcacaaa 1145
DB 1161 ctatgaagctgcacagatacagctatgttacttctgcgtctaga 1210

```

# RESULT 8

ABAO5044 standard; CDNA; 1476 BP.

ABAO5044:

22-FEB-2002 (first entry)

A thaliana jasmonic acid carboxyl methyltransferase coding sequence #2.

Jasmonic acid carboxyl methyltransferase; virus resistance;

Insect resistance; cold resistance; drought resistance; antifungal;

S-adenosyl-L-methionine: jasmonic acid carboxyl methyltransferase;

bacterial phytopathogen resistance; salt resistance; DMT;

antibacterial; antiviral; transgenic plant; ss.

Arabidopsis thaliana.

Key Location/Qualifiers

5'UTR 1..14

CDS 15..1184

3'UTR 1185..1476

Product="Jasmonic acid carboxyl methyltransferase"

MO200196549-A1.

20-DEC-2001.

05-JUN-2001; 2001MO-KR00953.

13-JUN-2000; 2000KR-0032365.





	PR	16-JUN-1999;	99US-0139453-	PR	13-AUG-1999;	99US-0148341-	PR	13-AUG-1999;	99US-0148555-	PR	13-AUG-1999;	99US-0148565-
	PR	17-JUN-1999;	99US-0139492-	PR	17-JUN-1999;	99US-0139492-	PR	13-AUG-1999;	99US-0148684-	PR	13-AUG-1999;	99US-0148684-
	PR	18-JUN-1999;	99US-0139454-	PR	18-JUN-1999;	99US-0139454-	PR	16-AUG-1999;	99US-0149368-	PR	16-AUG-1999;	99US-0149368-
	PR	18-JUN-1999;	99US-0139455-	PR	18-JUN-1999;	99US-0139455-	PR	17-AUG-1999;	99US-0149175-	PR	17-AUG-1999;	99US-0149175-
	PR	18-JUN-1999;	99US-0139456-	PR	18-JUN-1999;	99US-0139456-	PR	18-AUG-1999;	99US-0148426-	PR	18-AUG-1999;	99US-0148426-
	PR	18-JUN-1999;	99US-0139457-	PR	18-JUN-1999;	99US-0139457-	PR	20-AUG-1999;	99US-0149722-	PR	20-AUG-1999;	99US-0149722-
	PR	18-JUN-1999;	99US-0139458-	PR	18-JUN-1999;	99US-0139458-	PR	20-AUG-1999;	99US-0149723-	PR	20-AUG-1999;	99US-0149723-
	PR	18-JUN-1999;	99US-0139459-	PR	18-JUN-1999;	99US-0139459-	PR	22-AUG-1999;	99US-0149920-	PR	22-AUG-1999;	99US-0149920-
	PR	18-JUN-1999;	99US-0139460-	PR	18-JUN-1999;	99US-0139460-	PR	22-AUG-1999;	99US-0149920-	PR	22-AUG-1999;	99US-0149920-
	PR	18-JUN-1999;	99US-0139461-	PR	18-JUN-1999;	99US-0139461-	PR	22-AUG-1999;	99US-0149920-	PR	22-AUG-1999;	99US-0149920-
	PR	18-JUN-1999;	99US-0139462-	PR	18-JUN-1999;	99US-0139462-	PR	22-AUG-1999;	99US-0150566-	PR	22-AUG-1999;	99US-0150566-
	PR	18-JUN-1999;	99US-0139463-	PR	18-JUN-1999;	99US-0139463-	PR	26-AUG-1999;	99US-0150584-	PR	26-AUG-1999;	99US-0150584-
	PR	18-JUN-1999;	99US-0139464-	PR	18-JUN-1999;	99US-0139464-	PR	27-AUG-1999;	99US-0151065-	PR	27-AUG-1999;	99US-0151065-
	PR	21-JUN-1999;	99US-0139817-	PR	21-JUN-1999;	99US-0139817-	PR	27-AUG-1999;	99US-0151066-	PR	27-AUG-1999;	99US-0151066-
	PR	22-JUN-1999;	99US-0139899-	PR	22-JUN-1999;	99US-0139899-	PR	30-AUG-1999;	99US-0151303-	PR	30-AUG-1999;	99US-0151303-
	PR	23-JUN-1999;	99US-0140353-	PR	23-JUN-1999;	99US-0140353-	PR	31-AUG-1999;	99US-0151438-	PR	31-AUG-1999;	99US-0151438-
	PR	24-JUN-1999;	99US-0140354-	PR	24-JUN-1999;	99US-0140354-	PR	01-SEP-1999;	99US-0151930-	PR	01-SEP-1999;	99US-0151930-
	PR	28-JUN-1999;	99US-0140695-	PR	28-JUN-1999;	99US-0140695-	PR	07-SEP-1999;	99US-0152363-	PR	07-SEP-1999;	99US-0152363-
	PR	29-JUN-1999;	99US-0140823-	PR	29-JUN-1999;	99US-0140823-	PR	10-SEP-1999;	99US-0153070-	PR	10-SEP-1999;	99US-0153070-
	PR	30-JUN-1999;	99US-0140991-	PR	30-JUN-1999;	99US-0140991-	PR	13-SEP-1999;	99US-0153758-	PR	13-SEP-1999;	99US-0153758-
	PR	01-JUL-1999;	99US-0141842-	PR	01-JUL-1999;	99US-0141842-	PR	15-SEP-1999;	99US-0154018-	PR	15-SEP-1999;	99US-0154018-
	PR	02-JUL-1999;	99US-0142154-	PR	02-JUL-1999;	99US-0142154-	PR	16-SEP-1999;	99US-0154039-	PR	16-SEP-1999;	99US-0154039-
	PR	06-JUL-1999;	99US-0142055-	PR	06-JUL-1999;	99US-0142055-	PR	20-SEP-1999;	99US-0154473-	PR	20-SEP-1999;	99US-0154473-
	PR	08-JUL-1999;	99US-0142803-	PR	08-JUL-1999;	99US-0142803-	PR	22-SEP-1999;	99US-0155133-	PR	22-SEP-1999;	99US-0155133-
	PR	09-JUL-1999;	99US-0142920-	PR	09-JUL-1999;	99US-0142920-	PR	23-SEP-1999;	99US-0155486-	PR	23-SEP-1999;	99US-0155486-
	PR	12-JUL-1999;	99US-0143297-	PR	12-JUL-1999;	99US-0143297-	PR	28-SEP-1999;	99US-0156559-	PR	28-SEP-1999;	99US-0156559-
	PR	13-JUL-1999;	99US-0143542-	PR	13-JUL-1999;	99US-0143542-	PR	28-SEP-1999;	99US-0156458-	PR	28-SEP-1999;	99US-01

Oy	92	aatgacattcctaattctggcttgcgttcgaagaagtgaacctttcttggaacaatgatcaaga	151
Db	102	aactccaagtcagccgaatgatcatgcccgttcatcttcaaccctccttagaggaaacactt	161
Oy	152	gaattgttcggcgccgaacttcgcccaacaataaagaatgatthaagtctggatttggga	211
Db	162	gaaatgtctcaacttaactctcccgccagtcgcacccgttcacggcggttctgttcggc	221
Oy	212	tgcgcttcttgacccaacaacacttttaacagtcgcyggagatctgtgcgaagtattgaaa	271
Db	222	tgtctccctcggcgcaataactctgcacataatcogatattcataagtaaacatactctaa-	280
Oy	272	gttcgcacgaagaagaaytaalttagaacgtccccacatcagaattttctcgaatgat	331
Db	281	----gaagtttgttgctgcgcgaatcgaccctccggagttacaagctttctctccgat	335
Oy	332	cttttccaaatatgatattcattcagtttcttaagtctgtccaaagctt-----ctac	382
Db	336	ctcccaagaacagacttcaacacagcttttccagatctttcccaacttgccttaacact	395
Oy	383	cgcgaactcgcgaagaanaatgacgcacaagatagatcgtgcgtctaataagcgaatgact	442
Db	396	tgcattgagggagtgtctgtcgtcgcagcggaacgcgtcctacttcgttgtctgtcc	455
Oy	443	gagctcttctacagcacactctcccccgaagatgcattgatttgcactctgttac	502
Db	456	gagatcgtttatccgcgcgactttttccagcgcgaacacttgactttttccactgccttc	515
Oy	503	agagtcattcttgattatcattcaggttcccgagtcggttggatgattggagattgttga	562
Db	516	tctctgattcgtgcctctcctaagtcgcggaaagtgtgacgatagagatcgcggsggtac	575
Oy	563	aaacaaagggaattacc	580
Db	576	aataagggagaagatttc	593
<b>RESULT 10</b>			
AAC33567	standard; DNA; 1211 BP.		
ID AAC33567			
XX AAC33567;			
AC AAC33567;			
XX AAC33567;			
DT 17-OCT-2000	(first entry)		
XX 17-OCT-2000			
DE Arabidopsis thaliana DNA fragment SBO ID NO: 3524.			
XX Arabidopsis thaliana DNA fragment SBO ID NO: 3524.			
KV Hybridization assay; genetic mapping; gene expression control;			
KW protein identification; signal transduction pathway;			
KW metabolic pathway; promoter; termination sequence; ss.			
OS Arabidopsis thaliana.			
XX EPI033405-A2.			
PN EPI033405-A2.			
PD 06-SEP-2000.			
PF 25-FEB-2000; 2000EP-0301439.			
PR 25-FEB-1999; 99US-0121825.			
PR 05-MAR-1999; 99US-0123180.			
PR 09-MAR-1999; 99US-0123548.			
PR 23-MAR-1999; 99US-0125788.			
PR 23-MAR-1999; 99US-0126264.			
PR 29-MAR-1999; 99US-0126785.			
PR 01-APR-1999; 99US-0128734.			
PR 06-APR-1999; 99US-0128714.			
PR 16-APR-1999; 99US-0129645.			
PR 19-APR-1999; 99US-0130077.			
PR 21-APR-1999; 99US-0130049.			
PR 23-APR-1999; 99US-0130510.			
PR 23-APR-1999; 99US-0130891.			
PR 28-APR-1999; 99US-0131448.			
PR 30-APR-1999; 99US-0132048.			
PR 04-MAY-1999; 99US-0132407.			
PR 05-MAY-1999; 99US-0132485.			
PR 06-MAY-1999; 99US-0132486.			
PR 07-MAY-1999; 99US-0132487.			
PR 07-MAY-1999; 99US-0132483.			
PR 11-MAY-1999; 99US-0134256.			
PR 14-MAY-1999; 99US-0134218.			
PR 14-MAY-1999; 99US-0134219.			
PR 14-MAY-1999; 99US-0134370.			
PR 18-MAY-1999; 99US-0134768.			
PR 18-MAY-1999; 99US-0134841.			
PR 21-MAY-1999; 99US-0135124.			
PR 21-MAY-1999; 99US-0135353.			
PR 25-MAY-1999; 99US-0135629.			
PR 25-MAY-1999; 99US-0136692.			
PR 28-MAY-1999; 99US-0136782.			
PR 03-JUN-1999; 99US-0137528.			
PR 03-JUN-1999; 99US-0137724.			

```

PR 21-JUL-1999; 99US-0144814
PR 21-JUL-1999; 99US-0145086
PR 21-JUL-1999; 99US-0145088
PR 22-JUL-1999; 99US-0145085
PR 22-JUL-1999; 99US-0145087
PR 22-JUL-1999; 99US-0145089
PR 22-JUL-1999; 99US-0145192
PR 23-JUL-1999; 99US-0145145
PR 23-JUL-1999; 99US-0145224
PR 23-JUL-1999; 99US-0145224
PR 26-JUL-1999; 99US-0145276
PR 27-JUL-1999; 99US-0145913
PR 27-JUL-1999; 99US-0145918
PR 27-JUL-1999; 99US-0145919
PR 28-JUL-1999; 99US-0145951
PR 02-AUG-1999; 99US-0146386
PR 02-AUG-1999; 99US-0146388
PR 03-AUG-1999; 99US-0146389
PR 04-AUG-1999; 99US-0147204
PR 04-AUG-1999; 99US-0147302
PR 05-AUG-1999; 99US-0147192
PR 05-AUG-1999; 99US-0147260
PR 06-AUG-1999; 99US-0147303
PR 06-AUG-1999; 99US-0147416
PR 09-AUG-1999; 99US-0147493
PR 10-AUG-1999; 99US-0147935
PR 11-AUG-1999; 99US-0148171
PR 12-AUG-1999; 99US-0148319
PR 13-AUG-1999; 99US-0148341
PR 13-AUG-1999; 99US-0148365
PR 16-AUG-1999; 99US-0148684
PR 17-AUG-1999; 99US-0149175
PR 18-AUG-1999; 99US-0149426
PR 20-AUG-1999; 99US-0149722
PR 20-AUG-1999; 99US-0149723
PR 20-AUG-1999; 99US-0149929
PR 23-AUG-1999; 99US-0149902
PR 23-AUG-1999; 99US-0149930
PR 25-AUG-1999; 99US-0150864
PR 26-AUG-1999; 99US-0150884
PR 27-AUG-1999; 99US-0151065
PR 27-AUG-1999; 99US-0151066
PR 30-AUG-1999; 99US-0151080
PR 31-AUG-1999; 99US-0151303
PR 01-SEP-1999; 99US-0151338
PR 07-SEP-1999; 99US-0151363
PR 10-SEP-1999; 99US-0153700
PR 13-SEP-1999; 99US-0153758
PR 15-SEP-1999; 99US-0154018
PR 16-SEP-1999; 99US-0154039
PR 20-SEP-1999; 99US-0154179
PR 22-SEP-1999; 99US-0155139
PR 23-SEP-1999; 99US-0155486
PR 24-SEP-1999; 99US-0155659
PR 28-SEP-1999; 99US-0156458
PR 29-SEP-1999; 99US-0156596
PR 04-OCT-1999; 99US-0157117
PR 05-OCT-1999; 99US-0157753
PR 06-OCT-1999; 99US-0157865
PR 07-OCT-1999; 99US-0158029
PR 08-OCT-1999; 99US-0158322
PR 12-OCT-1999; 99US-0158369
PR 13-OCT-1999; 99US-0158393
PR 13-OCT-1999; 99US-0159294
PR 13-OCT-1999; 99US-0159295
PR 14-OCT-1999; 99US-0159329
PR 14-OCT-1999; 99US-0159330
PR 14-OCT-1999; 99US-0159331
PR 14-OCT-1999; 99US-0159637
PR 14-OCT-1999; 99US-0159638

```

```

PR 18-OCT-1999; 99US-0159584
PR 21-OCT-1999; 99US-0160741
PR 21-OCT-1999; 99US-0160767
PR 21-OCT-1999; 99US-0160768
PR 21-OCT-1999; 99US-0160770
PR 21-OCT-1999; 99US-0160814
PR 21-OCT-1999; 99US-0160815
PR 22-OCT-1999; 99US-0160980
PR 22-OCT-1999; 99US-0160981
PR 22-OCT-1999; 99US-0160989
PR 25-OCT-1999; 99US-0161404
PR 25-OCT-1999; 99US-0161405
PR 25-OCT-1999; 99US-0161406
PR 26-OCT-1999; 99US-0161359
PR 26-OCT-1999; 99US-0161360
PR 26-OCT-1999; 99US-0161361
PR 28-OCT-1999; 99US-0161920
PR 28-OCT-1999; 99US-0161921
PR 28-OCT-1999; 99US-0161992
PR 28-OCT-1999; 99US-0161993
PR 29-OCT-1999; 99US-0162142

```

Query Match 3.8% Score 48.8; DB 21; Length 1211;  
 Best Local Similarity 45.9%; Prod No. 0.0047;  
 Matches 256; Conservative 0; Mismatches 287; Indels 15; Gaps 2;

```

QY 32 atggagctccaaagaagtcctgcataatgaagaagtcgaagcgatcaagctcgcgaag 91
DB 46 atgaagctcgaagactcttcgcacatgaagaagtcgaagaagaagcagctcgcgaat 105
QY 92 aatgatccatcatctgctctctgcgaagtcgaaccttctccttgacatgacatgacga 151
DB 106 aactctcaagctcagcgaatgacatgacatgacatgacatgacatgacatgacatgac 165
QY 152 gaattgttcgagcgaactctgcgaacacacacacacacacacacacacacacacacac 211
DB 166 gaaatgttcacacacacacacacacacacacacacacacacacacacacacacacac 225
QY 212 tgcgctctgacacacacacacacacacacacacacacacacacacacacacacacac 271
DB 226 tcttcctcgcgcgaacacacacacacacacacacacacacacacacacacacacacac 284
QY 272 gtgtgcgaggaagaagaatgaatgaagaagtcgaagtcgaagtcgaagtcgaagtcga 331
DB 285 -----gaagttcgtcgcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcga 339
QY 332 ctttcacaaatcattcaatcgtgttcaagtgtgcgaagtc-----ctac 382
DB 340 cttcccaagcagcacttcaacacacacacacacacacacacacacacacacacacacac 399
QY 383 cgcacacgcgaagaagaatgaagaagaatgaagaatgaagaatgaagaatgaagaatgaaga 442
DB 400 tgcagagagagagtcctctgcgcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtc 459
QY 443 ggccttctcagcgaagtcctcccgagagtcgaatgacatgacatgacatgacatgacatgac 502
DB 460 ggaatgtttacgcgcgaacttcttcacagcgaagaacacatgacatgacatgacatgac 519
QY 503 atgtatcattgttatcaggttccacgcggttggatgacatgacatgacatgacatgacatgac 562
DB 520 tcttgcattgctcctcagtcgcgaagaagtcgaagaagaagtcgaagaagaatgcgcgagtc 579
QY 563 aacaaaggagatcttac 580
DB 580 aataagagagagatcttc 597

```

RESULT 11  
 ID AAS07727 standard; DNA; 198 BP.  
 AC AAS07727;  
 XX  
 DT 23-OCT-2001 (first entry)



PR 18-JUN-1999; 9905-0139457.  
 PR 18-JUN-1999; 9905-0139458.  
 PR 18-JUN-1999; 9905-0139459.  
 PR 18-JUN-1999; 9905-0139460.  
 PR 18-JUN-1999; 9905-0139461.  
 PR 18-JUN-1999; 9905-0139462.  
 PR 18-JUN-1999; 9905-0139463.  
 PR 18-JUN-1999; 9905-0139470.  
 PR 18-JUN-1999; 9905-0139473.  
 PR 21-JUN-1999; 9905-0138817.  
 PR 22-JUN-1999; 9905-0139899.  
 PR 23-JUN-1999; 9905-0140353.  
 PR 23-JUN-1999; 9905-0140354.  
 PR 24-JUN-1999; 9905-0140695.  
 PR 28-JUN-1999; 9905-0140823.  
 PR 29-JUN-1999; 9905-0140991.  
 PR 30-JUN-1999; 9905-0141287.  
 PR 01-JUL-1999; 9905-0141842.  
 PR 01-JUL-1999; 9905-0142154.  
 PR 02-JUL-1999; 9905-0142055.  
 PR 06-JUL-1999; 9905-0142390.  
 PR 08-JUL-1999; 9905-0142803.  
 PR 12-JUL-1999; 9905-0142920.  
 PR 13-JUL-1999; 9905-0142917.  
 PR 14-JUL-1999; 9905-0143342.  
 PR 15-JUL-1999; 9905-0143624.  
 PR 16-JUL-1999; 9905-0144005.  
 PR 16-JUL-1999; 9905-0144085.  
 PR 19-JUL-1999; 9905-0144325.  
 PR 19-JUL-1999; 9905-0144331.  
 PR 19-JUL-1999; 9905-0144332.  
 PR 19-JUL-1999; 9905-0144333.  
 PR 19-JUL-1999; 9905-0144334.  
 PR 19-JUL-1999; 9905-0144335.  
 PR 20-JUL-1999; 9905-0144352.  
 PR 20-JUL-1999; 9905-0144862.  
 PR 21-JUL-1999; 9905-0144864.  
 PR 21-JUL-1999; 9905-0144866.  
 PR 21-JUL-1999; 9905-0145008.  
 PR 22-JUL-1999; 9905-0145085.  
 PR 22-JUL-1999; 9905-0145087.  
 PR 22-JUL-1999; 9905-0145089.  
 PR 23-JUL-1999; 9905-0145192.  
 PR 23-JUL-1999; 9905-0145145.  
 PR 23-JUL-1999; 9905-0145218.  
 PR 23-JUL-1999; 9905-0145224.  
 PR 26-JUL-1999; 9905-0145276.  
 PR 27-JUL-1999; 9905-0145913.  
 PR 27-JUL-1999; 9905-0145918.  
 PR 27-JUL-1999; 9905-0145919.  
 PR 28-JUL-1999; 9905-0145951.  
 PR 02-AUG-1999; 9905-0146386.  
 PR 02-AUG-1999; 9905-0146388.  
 PR 03-AUG-1999; 9905-0146389.  
 PR 03-AUG-1999; 9905-0147038.  
 PR 04-AUG-1999; 9905-0147204.  
 PR 04-AUG-1999; 9905-0147302.  
 PR 05-AUG-1999; 9905-0147192.  
 PR 05-AUG-1999; 9905-0147260.  
 PR 06-AUG-1999; 9905-0147303.  
 PR 06-AUG-1999; 9905-0147416.  
 PR 09-AUG-1999; 9905-0147493.  
 PR 09-AUG-1999; 9905-0147935.  
 PR 10-AUG-1999; 9905-0148171.  
 PR 11-AUG-1999; 9905-0148319.  
 PR 12-AUG-1999; 9905-0148341.  
 PR 13-AUG-1999; 9905-0148565.  
 PR 13-AUG-1999; 9905-0148684.  
 PR 16-AUG-1999; 9905-0149388.  
 PR 17-AUG-1999; 9905-0149175.  
 PR 18-AUG-1999; 9905-0149426.

PR 20-AUG-1999; 9905-0149722.  
 PR 20-AUG-1999; 9905-0149723.  
 PR 20-AUG-1999; 9905-0149929.  
 PR 23-AUG-1999; 9905-0149902.  
 PR 23-AUG-1999; 9905-0149930.  
 PR 25-AUG-1999; 9905-0150366.  
 PR 26-AUG-1999; 9905-0150384.  
 PR 27-AUG-1999; 9905-0151065.  
 PR 27-AUG-1999; 9905-0151066.  
 PR 27-AUG-1999; 9905-0151080.  
 PR 30-AUG-1999; 9905-0151303.  
 PR 31-AUG-1999; 9905-0151348.  
 PR 01-SEP-1999; 9905-0151930.  
 PR 07-SEP-1999; 9905-0152363.  
 PR 10-SEP-1999; 9905-0153070.  
 PR 13-SEP-1999; 9905-0153758.  
 PR 15-SEP-1999; 9905-0154018.  
 PR 16-SEP-1999; 9905-0154039.  
 PR 20-SEP-1999; 9905-0154779.  
 PR 22-SEP-1999; 9905-0155139.  
 PR 23-SEP-1999; 9905-0155486.  
 PR 24-SEP-1999; 9905-0155959.  
 PR 28-SEP-1999; 9905-0156458.  
 PR 29-SEP-1999; 9905-0156596.  
 PR 04-OCT-1999; 9905-0157117.  
 PR 05-OCT-1999; 9905-0157753.  
 PR 06-OCT-1999; 9905-0157865.  
 PR 07-OCT-1999; 9905-0158029.  
 PR 08-OCT-1999; 9905-0158232.  
 PR 12-OCT-1999; 9905-0158369.  
 PR 13-OCT-1999; 9905-0159293.  
 PR 13-OCT-1999; 9905-0159294.  
 PR 13-OCT-1999; 9905-0159295.  
 PR 14-OCT-1999; 9905-0159329.  
 PR 14-OCT-1999; 9905-0159330.  
 PR 14-OCT-1999; 9905-0159331.  
 PR 14-OCT-1999; 9905-0159637.  
 PR 14-OCT-1999; 9905-0159638.  
 PR 18-OCT-1999; 9905-0159584.  
 PR 21-OCT-1999; 9905-0160741.  
 PR 21-OCT-1999; 9905-0160767.  
 PR 21-OCT-1999; 9905-0160768.  
 PR 21-OCT-1999; 9905-0160770.  
 PR 21-OCT-1999; 9905-0160814.  
 PR 21-OCT-1999; 9905-0160815.  
 PR 22-OCT-1999; 9905-0160980.  
 PR 22-OCT-1999; 9905-0160981.  
 PR 22-OCT-1999; 9905-0160989.  
 PR 25-OCT-1999; 9905-0161404.  
 PR 25-OCT-1999; 9905-0161405.  
 PR 26-OCT-1999; 9905-0161406.  
 PR 26-OCT-1999; 9905-0161359.  
 PR 26-OCT-1999; 9905-0161360.  
 PR 26-OCT-1999; 9905-0161361.  
 PR 28-OCT-1999; 9905-0161920.  
 PR 28-OCT-1999; 9905-0161922.  
 PR 28-OCT-1999; 9905-0161993.  
 PR 29-OCT-1999; 9905-0162142.

Query Match 3.3%; Score 42.6; DB 21; Length 1259;  
 Best Local Similarity 53.3%; Pred. No. 0.22;  
 Matches 90; Conservative 0; Mismatches 79; Indels 0; Gaps 0;  
 Oy 412 gatagatcgcgtactaagaagcaatgcgtctcttcttaagcgaagactcttcccca 471  
 Db 405 gaaccgcctcactcttgctgcgtggtcccgatcggttcaacggacttttccagc 466  
 Oy 472 gaagccatgcatttttgcactcttgtaagtgtaactatgtgtatctcaagttccca 531  
 Db 465 gaagacatgcacttttccactcttcctctccttgatgtgctctcctcaagttccgga 524  
 Oy 532 cggattggtgatitgaaltggggatggtgtaacaacaaggagattttac 580

Db 525 aagtgatgacgagatgacgagcgcgcgcacacatagaggagagcttttc 573  
RESULT 13  
ID AAC36551 standard; DNA; 1261 BP.  
AC AAC36551;  
XX 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 14222.  
DE  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
OS  
PN BP103405-A2.  
XX  
PD 06-SEP-2000.  
XX  
DF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136682.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 13-JUL-1999; 99US-0143634.  
PR 16-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144006.  
PR 16-JUL-1999; 99US-0144008.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 21-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147492.  
PR 09-AUG-1999; 99US-0147932.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.

```

PR 18-AUG-1999; 99US-0149426
PR 20-AUG-1999; 99US-0149722
PR 20-AUG-1999; 99US-0149723
PR 20-AUG-1999; 99US-0149929
PR 23-AUG-1999; 99US-0149902
PR 23-AUG-1999; 99US-0149930
PR 25-AUG-1999; 99US-0150566
PR 26-AUG-1999; 99US-0150884
PR 27-AUG-1999; 99US-0151085
PR 27-AUG-1999; 99US-0151086
PR 27-AUG-1999; 99US-0151087
PR 30-AUG-1999; 99US-0151303
PR 31-AUG-1999; 99US-0151438
PR 01-SEP-1999; 99US-0151930
PR 07-SEP-1999; 99US-0152363
PR 10-SEP-1999; 99US-0153070
PR 13-SEP-1999; 99US-0153758
PR 15-SEP-1999; 99US-0154018
PR 16-SEP-1999; 99US-0154039
PR 20-SEP-1999; 99US-0154779
PR 22-SEP-1999; 99US-0155139
PR 23-SEP-1999; 99US-0155486
PR 24-SEP-1999; 99US-0155659
PR 28-SEP-1999; 99US-0156458
PR 29-SEP-1999; 99US-0156596
PR 04-OCT-1999; 99US-0157117
PR 05-OCT-1999; 99US-0157253
PR 06-OCT-1999; 99US-0157865
PR 07-OCT-1999; 99US-0158028
PR 08-OCT-1999; 99US-0158232
PR 12-OCT-1999; 99US-0158359
PR 13-OCT-1999; 99US-0159223
PR 13-OCT-1999; 99US-0159224
PR 13-OCT-1999; 99US-0159285
PR 14-OCT-1999; 99US-0159329
PR 14-OCT-1999; 99US-0159330
PR 14-OCT-1999; 99US-0159331
PR 14-OCT-1999; 99US-0159637
PR 14-OCT-1999; 99US-0159638
PR 18-OCT-1999; 99US-0159584
PR 21-OCT-1999; 99US-0160741
PR 21-OCT-1999; 99US-0160767
PR 21-OCT-1999; 99US-0160770
PR 21-OCT-1999; 99US-0160814
PR 21-OCT-1999; 99US-0160815
PR 22-OCT-1999; 99US-0160980
PR 22-OCT-1999; 99US-0160981
PR 25-OCT-1999; 99US-0161405
PR 25-OCT-1999; 99US-0161406
PR 25-OCT-1999; 99US-0161407
PR 26-OCT-1999; 99US-0161359
PR 26-OCT-1999; 99US-0161360
PR 26-OCT-1999; 99US-0161361
PR 28-OCT-1999; 99US-0161920
PR 28-OCT-1999; 99US-0161922
PR 28-OCT-1999; 99US-0161993
PR 29-OCT-1999; 99US-0162142

```

Query Match 3.3%; Score 42.6; DB 21; Length 1261;  
 Best Local Similarity 5.3%; Pred. No. 0.22;  
 Matches 90; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

```

OY 412 gatagatcgttcacaaatagcgaatgctgctcttcttaacgacgaactctccaga 471
    || || || || || || || || || || || || || || || || || || || ||
Db 407 gaacgcctcctactcgtcgtcgttcccgatcgcttttaacggtaacttttccagc 466
OY 412 ggaatcgaatctttttgacatctgttaacggttcattgtaattcgaagttccag 531
    || || || || || || || || || || || || || || || || || || || ||
Db 467 gagaacatctgacttttccacacgcctctcctctgcatctgacgtccctcaggtccgaga 526
OY 532 cggattggtgattgaattggggtggtggtgacaaacaaaggagattattac 580

```

Db 527 aagttgacgagatagagatcgcgcgcgtacataagaggagagtttcc 575

#### RESULT 14

ID AAX60802 standard; DNA; 3637 BP.

AAX60802;

09-AUG-1999 (first entry)

Human secreted protein encoding DNA (clone f3283-11).

Secreted protein; kidney; lung; brain; blood; testis; bone marrow;

nutritional activity; cytokine; cell proliferation; immune stimulation;

hematopoiesis regulation; tissue growth; thrombolytic; gene therapy;

anti-inflammatory; tumour invasion; ss.

Homo sapiens.

W09926961-A1.

03-JUN-1999.

24-NOV-1998; 98MO-US25149.

23-NOV-1998; 98US-0197886.

26-NOV-1997; 97US-0066804.

(GENM ) GENETICS INST INC.

Agostino MJ, Clark HF, Collins-Racie LA, Evans C;

Rechtel K, Jacobs K, Lavallie ER, McCoy JM, Merberg D;

Steininger RJ, Treacy M, Wong GG;

WPI: 1999-357809/30.

P-PSDB; AAY17220.

New polynucleotides encoding secreted proteins

Disclosure: Page 113-114; 133pp; English.

The invention relates to secreted proteins (AAY17219-228) encoded by

polynucleotides obtained from human fetal kidney, adult lung, adult

kidney, adult brain, adult blood, adult testes, and fetal brain and

murine adult bone marrow cDNA libraries. The secreted protein nucleic

acid sequences (X6801-811) correspond to clones D0306-7, 9J283-6,

IK317-3, K213-2x, na16-1, n193-20, nP164-1, pe204-1, and yd-1.

(all clones are deposited as ATCC 98599). The PNs and proteins are

predicted to have biological activities which would make them suitable

for treating, preventing or ameliorating medical conditions in humans and

animals, although no supporting data is given. Suggested activities

include nutritional activity, cytokine and cell

proliferation/differentiation activity, immune stimulating (e.g. as

vaccines) or suppressing activity, hematopoiesis regulating activity,

tissue growth activity, activin/inhibin activity,

chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,

receptor/ligand activity, anti-inflammatory activity, cadherin/tumour

invasion suppressor activity, and tumour inhibition activity. The PNs are

also stated to be useful for gene therapy.

Sequence 3637 BP; 1132 A; 598 C; 837 G; 1069 T; 1 other;

#### Query Match

Best Local Similarity 3.2%; Score 41.4; DB 20; Length 3637;  
 Matches 72; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

```

OY 1176 ttcttagtcttttttgcgcgttgggggtctcttcgggtaattgcttttgatcgttaa 1235
    || || || || || || || || || || || || || || || || || || || ||
Db 3487 ttcttgtaactttctgttttgcgcgttgggggtctcttcgggtaattgcttttgatcgttaa 3546

```

QY 1236 taaagtgatgcaagaataatattagtaacattttccataaaaaaaaaa 1295  
 DB 3547 taatgtacacataaaggttaacatttttaagtgaataaaaaaaaaa 3606  
 QY 1296 aaa 1298  
 DB 3607 aaa 3609  
 RESULT 15  
 AAS59208  
 ID AAS59208 standard; cDNA; 3637 BP.  
 AC AAS59208;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE Human cDNA encoding a secreted protein f3283\_11.  
 XX  
 KM Human; secreted protein; ss; antiinflammatory; immunosuppressive;  
 KM neotropic; neuroprotective; antiarthritic; antimicrobial; vulnery;  
 KM cytostatic; antidiabetic; virucide; antifertility; anticonvulsant;  
 KM vasotropic; antiparkinsonian; immunostimulant; dermatological;  
 KM antihemagic; antitumor; antilucer; osteopathic; tranquiliser;  
 KM cerebroprotective; cytokine; cell proliferation; cell differentiation;  
 KM immune deficiency; severe combined immunodeficiency; SCID; tumour;  
 KM autoimmune disorder; multiple sclerosis; rheumatoid arthritis;  
 KM graft-versus-host disease; myeloid deficiency; wound healing; ulcer;  
 KM periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;  
 KM Parkinson's disease; Huntington's disease; infection; cardiac disease;  
 KM stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;  
 KM food supplement.  
 XX  
 OS Homo sapiens.  
 XX  
 PN NC0200175068-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 22-MAR-2001; 2001MO-US09369.  
 XX  
 PR 30-MAR-2000; 2000US-0539330.  
 PR 04-DEC-2000; 2000US-0729674.  
 XX  
 PA (GENY) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie E, Collins-racle LA, Evans C;  
 PI Treacy M, Agostino MJ, Steininger RJ, Spaulding V, Wong GG;  
 PI Clark H, Fechtel K, Werberg D;  
 XX  
 DR WPI; 2001-639363/73.  
 DR P-PSDB; NAU38990.  
 XX  
 PT Secreted human proteins, useful as vaccine for treating various  
 PT diseases such as autoimmune disorders (e.g. multiple sclerosis), and  
 PT nervous system disorders (e.g. stroke).  
 XX  
 PS Disclosure; Page 459-460; 619p; English.  
 XX  
 CC The invention relates to novel human secreted proteins, the nucleic  
 CC acids encoding them. The protein may exhibit cytokine, cell proliferation  
 CC or cell differentiation activity or may induce production of other  
 CC cytokines in certain cell populations and may exhibit immune stimulating  
 CC or immune suppressing activity, which is useful for the treatment of  
 CC various immune deficiencies and disorders e.g. severe combined  
 CC immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis,  
 CC systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary  
 CC inflammation. The proteins are also useful in the treatment of diseases  
 CC and disorders including tissue, skin and organ transplantation and in  
 CC graft-versus-host diseases (GVHD). In the induction of tumour immunity,  
 CC myeloid or lymphoid cell deficiencies, wound healing and tissue repair.  
 CC In the treatment of burns, incisions and ulcers, as well as in treatment  
 CC of periodontal disease, osteoporosis or osteoarthritis, mediated by

CC inflammatory processes, diseases of the peripheral nervous system,  
 CC Alzheimer's Parkinson's disease, Huntington's disease,  
 CC amyotrophic lateral sclerosis, and Shy-Drager syndrome, infections,  
 CC infection of cardiac and central nervous system vessel e.g. stroke,  
 CC sepsis, inflammatory bowel disease, ulcers, bone regeneration. The  
 CC protein, having activity or inhibin-related activities is useful as a  
 CC contraceptive based on the ability of inhibins to decrease fertility in  
 CC female mammals and decrease spermatogenesis in male mammals. The  
 CC proteins and nucleic acids are also useful as food supplements. The  
 CC present sequence encodes a secreted protein of the invention.  
 XX  
 SQ Sequence 3637 BP; 1132 A; 598 C; 837 G; 1069 T; 1 other;

Query Match 3.2%; Score 41.4; DB 22; Length 3637;  
 Best Local Similarity 58.5%; Pred. No. 0.72;  
 Matches 72; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
 QY 1176 ttttaagtgattttgtcgcgttgagggtcttcggggtatgctgtttgtatcgtaa 1235  
 DB 3487 tttttgtgactttgtttgtcgttgagggtcttcggggtatgctgtttgtatcgtaa 3546  
 QY 1236 taaagtgatgcaagaataatattagtaacattttccataaaaaaaaaa 1295  
 DB 3547 taatgtacacataaaggttaacatttttaagtgaataaaaaaaaaa 3606  
 QY 1296 aaa 1298  
 DB 3607 aaa 3609

Search completed: July 27, 2002, 04:45:04  
 Job time: 4660 sec



---









```

CDS
14..1171
/ gene="Camt1L"
/ locus="Camt1L"
/ product="caffeine synthase"
/ protein_id="BAB3213.1"
/ db_xref="GI:1336594"
/ translation="MELOEVLHMHNGEGEASNAKSSFNOLVAKKPYLEDCVRELL
RAULPINKICIVADLCASPNLITVMDVLOSIDKVKOMKNELEPPIOVFTDL
FONDFNSVFMLEPSFYRLKLEKENGRIKISCLIAAPGSGFNGRLPEESMHFLHSYSL
QFISQVPSGLVLELIDANKRSIYSSKASPPVQAYADQTKPTFLMSBELLS
RGMILTICIKGDECDGNPTMDLEMAINDLVAEGRLEEDLSEFNVPITYTASVEVK
CMVEEGSEFELYLOTEFLRYDAGFSIDDCQVRSHPVSDEIARAHVASISIVY
EPLASHFEFALIPDIHFRFRAVNAVIRLGGFNNIILSLAKPEKSDI"
BASE COUNT
397 a 266 c 296 g 401 t
ORIGIN
Query Match 74.5% Score 966.6; DB 8; Length 1360;
Best local similarity 88.9%; Pred. No. 4,4e-239;
Matches 1076; Conservative 0; Mismatches 114; Indels 21; Gaps 2;
OY 19 gtccgcataatgagatgcacaaagaatcttcacataatgaagatgagagagatc
DB 1 gtccgcataatgagatgcacaaagaatcttcacataatgaagatgagagagatc
OY 79 aagctacgcaagaatgcatacaat---ctggctctgcgaagtgaaagcttctc
DB 61 aagctacgcaagaatgcatacaat---ctggctctgcgaagtgaaagcttctc
OY 136 tgaacaatgacataagaaatgtgtgcggcaacttgcacaatcaaaatgacataa
DB 121 tgaacaatgacataagaaatgtgtgcggcaacttgcacaatcaaaatgacataa
OY 196 agtgcggaatgtggatgcctctgcgaacaacacacttcaacagtcggagacatgt
DB 181 agtgcggaatgtggatgcctctgcgaacaacacacttcaacagtcggagacatgt
OY 256 gcaaatgttcaacaagtgtgcgaagaagaagaatgaatgaacgcgcacacattca
DB 241 acaaatgttgcacaaagtgtgcgaagaagaagaatgaatgaacgcgcacacattca
OY 316 gatttctgaaatgctcttcgaacaatgattcagttcagtttcaagtcgcgaag
DB 301 gatttctgaaatgctcttcgaacaatgattcagttcagtttcaagtcgcgaag
OY 376 ctctacacgcaaaatgcagaagaagaagaatgagacagatgcctgcataaagc
DB 361 ctctacacgcaaaatgcagaagaagaagaatgagacagatgcctgcataaagc
OY 436 aatgcctgctctcttcaaggagactctcccgagagatcagtcattttgcactc
DB 421 aatgcctgctctcttcaaggagactctcccgagagatcagtcattttgcactc
OY 496 ctgttacaagtctcatgttactcaggttcccgaggtttgtgtgattgaattggagat
DB 481 ctgttacaagtctcatgttactcaggttcccgaggtttgtgtgattgaattggagat
OY 556 tgggtgcaaaagaagagatcttacccttcacaaagatgtgcgcgcgcgcgcgaagc
DB 541 tgggtgcaaaagaagagatcttacccttcacaaagatgtgcgcgcgcgcgcgaagc
OY 616 aatttggatcaatttgaagaatttccacatttgaagaatttccacgaagatt
DB 601 aatttggatcaatttgaagaatttccacatttgaagaatttccacgaagatt
OY 676 gttttagatgagcgaatgtccttaccctgcagatgtgaagtagaatttgaagaac
DB 661 gttttagatgagcgaatgtccttaccctgcagatgtgaagtagaatttgaagaac
OY 736 gaattcccttagactactgcacatggaataaagaactgtgttgaagacttcgga
DB 721 gaattcccttagactactgcacatggaataaagaactgtgttgaagacttcgga

```

```

OY 796 ggaagaagaattgataatgattcaattcattcatttaacattcagagaagaataa
DB 781 ggaagaagaattgataatgattcaattcattcatttaacattcagagaagaataa
OY 856 gtgcattgttgaagagaaggtctcttcgaatttataatcctgagactttgaagcca
DB 841 gtgcattgttgaagagaaggtctcttcgaatttataatcctgagactttgaagcca
OY 916 ttatgattgtcctctctcattatgatgatattaccagaataatcc-----
DB 901 ttatgattgtcctctctcattatgatgatattaccagaataatcc-----
OY 963 -----atgaacaataaagaagatgtgtgcataatcaatgaatgaatttgaagc
DB 961 cagcattgacatgcatgacagacagcagcagcagcagcagcagcagcagcagc
OY 1018 catcctgcgaagctcatttggagaagcattatgcctgacttccacagacttcgaa
DB 1021 catcctgcgaagctcatttggagaagcattatgcctgacttccacagacttcgaa
OY 1078 gcatgagaagaagttcttcacatggaagaagctgctataatccttctctct
DB 1081 gcatgagaagaagttcttcacatggaagaagctgctataatccttctctct
OY 1138 ggcacaagaagcagaagatcagacagtgtaaaagttgttttagttgtgtgcgcg
DB 1141 tgcacaaaacacagacagatcagacatgtaaaagctgttttagttgtgtgtrra
OY 1198 ttggaggggtcctt 1208
DB 1201 ttggaggggtcctt 1211

RESULT 5
AB049752 1437 bp mRNA linear PLN 16-MAR-2001
LOCUS
DEFINITION
AB049752
AB049752
AB049752.1 GI:13366160
VERSION
KEYWORDS
SOURCE
ORGANISM
Atropa belladonna (strain:M8) root cDNA to mRNA, clone:lambda
ABSAMT1.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Solanales; Solanaceae; Atropa.
REFERENCE
1 (sites)
Fukami,H., Asakura,T., Hirano,H., Abe,K., Shimomura,K. and
Yamakawa,T.
Cloning and expression of salicylic acid inducible and active
S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase
in transformed root culture of Atropa belladonna
Unpublished
JOURNAL
2 (pages 1 to 1437)
REFERENCE
Fukami,H., Asakura,T., Hirano,H., Abe,K., Shimomura,K. and
Yamakawa,T.
Direct Submision
Submitted (10-OCT-2000) Takashi Yamakawa, The University of Tokyo,
Department of Global Agricultural Sciences, 1-1, Yayoi 1-chome,
Bunkyo-ku, Tokyo 113-8657, Japan
(E-mail:yamakawa11.ecc.u-tokyo.ac.jp, Tel:81-3-5841-7515,
Fax:81-3-5841-5304)
FEATURES
location/Qualifiers
1..1437
/organism="Atropa belladonna"
/strain="M8"
/db_xref="taxon:33113"
/clone="lambda ABSAMT1"
/tissue="root"
62..1135
gene

```

Query Match	Similarity	Score	ID	Length
Best Local Similarity	55.7%	176.4	DB 8	1437
Best Local Similarity	55.7%	Pred. No. 7.1e-35		
Matches	508	Conservative	0	Mismatches 356; Indels 48; Gaps 7

  

Query	Match	Similarity	Score	ID	Length
31	aatgagatcccaagaatcctgataataaagaagaggaagcgatacaagtaagccaa	90			
61	aatgaagctgttgaattcttctacataaaggaagaatgacatattgataagcaca	120			
91	gaatgc---atcccaaatctgctctcttgcagaagtgaaccttcccttgacaatgcat	147			
121	caattctctgcttcaggaagaagtaattctctatgacaaagcattatgacaaagccat	180			
148	acgagaatgtgtcggcgcaacttcgccaacatcacaagaatgcatataaagtctggatt	207			
181	aatgtatctctactgacagctctgttcccgaaaa-----cctttatgattgctgatt	231			
208	ggatgtgcctcttgcaccaaacacatttaacagtcggagacattgttgcagaatgtga	267			
232	gggtgtgtcttccggacacgaacatttttgggtgtatcgaacattgtttaatgttcga	291			
268	caaatgttgcagaagaagaagaatgaattgaatgaagtcgccacatcagaattttctgaa	327			
292	aaaaaagaaaaaaatgacatattcttgcacgacggg-----aatcttttccattcca	345			
328	tgatcttcccaaatatttcaatctcgatttcaagtctgcagaagcttcaacga	387			
346	tgatcttccctggcgaatgatttttmacccatttttcacgtatcttgggaattttcaacaga	405			
388	actcgagaagaataatgacgaagaatgagctctgctcctaataagtcgaatcctgcgtc	447			
406	tttgagaagaacaaattggaagaattttgttcacatgttttttaagtgagagtcctggtc	465			
448	tttcaaggagacatcttcccgagagatcacaatcttttgcacatctgttaagatgt	507			
466	atttttatcagacttttccctccagagaagtttgcattttgtcactccagttatagctc	525			
508	taattgtatcactgaattcccaagcggttggatgtgaatttggagattgtgtgcaaca	567			
526	catgtgcctatctacaaatttc-----taatttttaattaaaa-----gaacaa	567			
568	aggaagatcttaactcttccaaagaatgtcgcgcgcgcgcgcgaagaacatattgtatca	627			
568	ggaggaacattttacattgacagtaacagtcacaaagtttttaaaagcattactacaaaga	627			
628	attcaagaagaatttaccacatcttcaagaattcatttcgaagaagttgttttaacgtg	687			
628	atracaaataaataatttttcaaattttctcaaatatccgttgcaggaattttatgaagaagtcg	687			
688	cgaatgtccttaactcgtcaattgttaagatgatga-----ttcgaacacgaatcc	742			
688	gaataattgttttaacatttttaagaagaagaaggaagacattcttaccagaagaatctgt	747			
743	ctagaactacttga-----catgacataaagacattgtatgttgaagaacttccga	795			

```

Query Match      13.0%   Score 169, DB 8; Length 115;
Best Local Similarity 12.9%   Pred. No 5, Re-33;
Matches 557; Conservative 0; Mismatches 445; Indels 51; Gaps 7;

QY      32 atgagatcccaaaatcctgataatgaaatgaagtgaaagcgatacaagtaagcaaa 91
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       29 atgcaagatgtgtgaagttctttacatgaatgtagcaccctgagaattcgaagt 80

```

[illegible]

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	FEATURES
Cucumis sativus ERAF16 mRNA for S-adenosyl-L-methionine:sallylic acid calboxyl methyltransferase-like protein, complete cds.	AB046595			AB046595.1 GI:18461099	Cucumis sativus (cultivar:Shimoshirazu-1jibai) shoot apex cDNA to mRNA	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae; eustroids 1; Cucurbitales; Cucurbitaceae; Cucumis: 1 (bases 1 to 1308)	Direct Submission	Submitted (26-JUL-2000) Sugihito Ando, University of Tsukuba, Institute of Biological Sciences, Tennoudai 1-1-1, Tsukuba, Ibaraki 305-8572, Japan (E-mail: Sugihito@tsukuba.ac.jp, tsukuba.ac.jp, Tel:81-298-4871(ex.4871), Fax:81-298-4579)	Location/Qualifiers 1..1308 /organism="Cucumis sativus" /cultivar="Shimoshirazu-1jibai" /db_xref="taxon:3659" /tissue_type="shoot apex" 32..1144 /gene="ERAF16" 32..1144 /gene="ERAF16" /codon_start=1 /product="S-adenosyl-L-methionine:sallylic acid calboxyl methyltransferase-like protein" /protein_id="BAB84353.1" /db_xref="GI:18461100"
Query Match	12.28;	Score 157.8;	DB 8;	Length 1308;					
Best Local Similarity	52.28;	Pred. No. 4.5e-30;							
Matches 481; Conservative	0;	Mismatches 392;	Indels 48;	Gaps 4;					
OY 177	acatcaacaagtgaatcaagttgcggatttggaatcgcgcttccttgaccacaacacattc	236							
Db 156	ACATTTCACACATCATCACTAATCACTATGACGAGATTGGTGTCTTCAGACACAAACACTGTAA	215							
OY 237	taacagtcgcggaacatctgtcgaagaatgtgaacaagcttgcgcgagaagaagaatgaat	296							
Db 216	TGCTTCTTCTTACTACTGATCAACAACAGTCGAGTGAAGATTCCGC---AAAGCTTCACCAA	272							
OY 297	tagaagctcccccaccatccagattttcttgaaatgatcttcccaaatgatttcgaattcgg	356							
Db 273	GGCTGCCCTTGGAGATCAACAATCTTCTTGAAGATCTTCACGGAATGACTTCAATCTCG	332							
OY 357	tttccaagtctgcgcaagcttaccgcaaacctcgagaagaagaatgtgaacgaagaatag	416							
Db 333	TCTTTACATCATCAACAAAGTTTGGAGAGATTGGGAGCCAAATGAGAGTGATTTTG	392							
OY 417	gacgcgcctaaagaacgaacgtcgcgcgtctcttcacgcacacgtcccggaagagt	476							
Db 393	GTCCATGTTTCTCAAGGAGTCCCGGTTCTTTCATGCCAATCTTTGCCACAA	452							
OY 477	ccatgcatcttttgacactctgttacagtgatcatcttgatctcaggtccagcggt	536							
Db 453	GTGTTCATTTTTCATATCAATCAAGTAGAGCTTCATGAGCTTCTCGGGTTC-----	504							
OY 537	tgtgtgttaaatgaggatctgtgtgaacaagaaggagtatcttacccttccaaagaatgct	596							





```

Db 867 GATAAATTGACACCTTCATATACCCAGTATTTGCTGCTGCTGAGGAGGACAAAGAT 926
OY 860 atagttgaggaaggttcttcggaatttatactcggagactttaa 909
Db 927 ATATGTGAGAGGAGGATCATTCATATGATCATATGAGGGGTTGA 976

RESULT 9
LOCUS AX138776 1427 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 2 from Patent EP1055727.
ACCESSION AX138776
VERSION AX138776.1 GI:14274532
KEYWORDS
SOURCE
ORGANISM Camellia sinensis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Theaceae; Camellia.
1 (bases 1 to 1427)
REFERENCE Mizuno,M., Ashihara,H., Mizuno,K. and Fujimura,T.
AUTHORS Cloning of an n-methyltransferase involved in caffeine biosynthesis
JOURNAL Patent: EP 1055727-A.2 28-NOV-2000;
MITSUI CHEMICALS, INC. (JP)
FEATURES
source
1. 1427
/organism="Camellia sinensis"
/db_xref="taxon:4442"
BASE COUNT 444 a 251 c 330 g 402 t
ORIGIN

Query Match 10.7%; Score 138.8; DB 6; Length 1427;
Best Local Similarity 51.8%; Pred. No. 3.7e-25;
Matches 461; Conservative 0; Mismatches 392; Indels 37; Gaps 5;

OY 34 ggaagtcgaagaagtcctgcataatgaatgaaggcgaatgaagcgaaga 93
Db 80 GAAGTGAAGCAAGTGTTCATGAAACAGGGGGAAGGAAAGATATGCAAAA 139
OY 94 tgatcctcaactcgcgtctgc--caagtgaaaccttcctgaacaatgaaga 151
Db 140 CTCTCTTTCAGCAAAAGTGGCTCATATGGCAGCAGCGCTTGAATAATGGA 199
OY 152 gaattgttcgggccaacttgcacaatacaagaatgataaagttggattgga 211
Db 200 AACTCTCTTCACAGATTTTC-----ACCTTCAAGCTTTAAGCAGGACTGGCT 254
OY 212 tgcgtcttcggaacaacacctttaacagtcggggaactgtgcagaatgaaga 271
Db 255 TGTGACAGCGGTCCAAACACATTCGACATATTTTACGATCAAGAAATGATGAAAAG 314
OY 272 gtggccgaagaagaagaatgaatgaatgaacgctccacacatcagaattttcgaatgat 331
Db 315 AAATGCAAGGAATTTGA-----ATTGCCAAACACTGGAACCTTCAGCTTAACTGAAATGAT 368
OY 332 ctttccaaaatgaatcgaatcgaatttcgaagtgtcgcgaagcttcaacgcaaatc 391
Db 369 CTTTGTGAAATGATTTCAATCCCTCTTCAAAAGCGCTGCGCTGAG----- 416
OY 392 gagaagaagaatgagaagaatgagatcgctgcaataaagcgaatgcgtccttc 451
Db 417 GTTATGTGTAACAAATGAGAGAAATTCCTGCTTATGATGATGAGATACCGGCGCTTTC 476
OY 452 taaggcgaactctcccggaagagtcacatgatttttgacactgtgaagtgat 511
Db 477 CATGGCGGCTTTTCTCTGTAACAGCTTACATTTAATTTCTCTTCAAGGTTTAT 536
OY 512 tgcattatcgaagttccagcggttggatgtaattggaggttcgggcaacaagg 571
Db 537 TGGTCTACTACGACCAAAAGGACTCACAAGCAGAGAGAAGGCTTGGCTTAATAAGGGG 596

```

```

OY 572 agtattactctccaaagagatgtcgcgccgcgcgaaggaacatattgatactt 631
Db 597 AAGATTTCATATCAAAAGACAGCCCTCTGTTGTAAGAGAGAGCTTACTCATATT 656
OY 632 acgaagaatttaccacatttcaagatcattcgaagaagtggtttcgaagtcga 691
Db 657 CATGAAGATTTCACAAATGTTTCTCATATGCTAGATCCAAAGGCTGTTCAATGTTGT 716
OY 692 atgccttaccgcgcatgtgtgaagtagat-----gaatgcgaacccaat 739
Db 717 ATGGGTGTAATCTTCGTGTGAGCAATTTCTGATCTTCAGACATGACAGACTGCTTT 776
OY 740 cccctgagcttactgcacatgcaataaagacattgattgttgaggacttcggagga 799
Db 777 ACTTGGAATCTATTAGCTATGCTATGGCCATTGCTGAAATTTGTTTCACAGGATGATGATGA 836
OY 800 gaaatattgataagtttcaatcattcattacaccttcaacattcagaagaagaatgac 859
Db 837 GATTAATTTAGACACCTTCATATATACCCAGCTATTTTGCATCATCTTGAGAGAAAGAT 896
OY 860 atagttgaggaaggttcttcggaatttatactcggagactttaa 909
Db 897 ATATGTGAGAGGAGGATCATTCATATGATCATATGAGGGGTTGA 946

RESULT 10
LOCUS AX138777 1427 bp mRNA linear PAT 30-MAY-2001
DEFINITION Sequence 3 from Patent EP1055727.
ACCESSION AX138777
VERSION AX138777.1 GI:14274533
KEYWORDS
SOURCE
ORGANISM Camellia sinensis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Theaceae; Camellia.
1 (bases 1 to 1427)
REFERENCE Mizuno,M., Ashihara,H., Mizuno,K. and Fujimura,T.
AUTHORS Cloning of an n-methyltransferase involved in caffeine biosynthesis
JOURNAL Patent: EP 1055727-A.3 29-NOV-2000;
MITSUI CHEMICALS, INC. (JP)
FEATURES
source
1. 1427
/organism="Camellia sinensis"
/db_xref="taxon:4442"
BASE COUNT 444 a 251 c 330 g 402 t
ORIGIN

Query Match 10.7%; Score 138.8; DB 6; Length 1427;
Best Local Similarity 51.8%; Pred. No. 3.7e-25;
Matches 461; Conservative 0; Mismatches 392; Indels 37; Gaps 5;

OY 34 ggaagtcgaagaagtcctgcataatgaatgaaggcgaatgaagcgaaga 93
Db 80 GAAGTGAAGCAAGTGTTCATGAAACAGGGGGAAGGAAAGATATGCAAAA 139
OY 94 tgatcctcaactcgcgtctgc--caagtgaaaccttcctgaacaatgaaga 151
Db 140 CTCTCTTTCAGCAAAAGTGGCTCATATGGCAGCAGCGCTTGAATAATGGA 199
OY 152 gaattgttcgggccaacttgcacaatacaagaatgataaagttggattgga 211
Db 200 AACTCTCTTCACAGATTTTC-----ACCTTCAAGCTTTAAGCAGGACTGGCT 254
OY 212 tgcgtcttcggaacaacacctttaacagtcggggaactgtgcagaatgaaga 271
Db 255 TGTGACAGCGGTCCAAACACATTCGACATATTTTACGATCAAGAAATGATGAAAAG 314
OY 272 gtggccgaagaagaagaatgaatgaatgaacgctccacacatcagaattttcgaatgat 331
Db 315 AAATGCAAGGAATTTGA-----ATTGCCAAACACTGGAACCTTCAGCTTAACTGAAATGAT 368

```



	DB	987	ATATGAGGAGGAGGACGATCATTTCAACAATTGCATTCATCATCTATGAGGGCGTTTGA	946
RESULT	12			
BD004679	BD004679	1427 bp	RNA	linear
LOCUS	DEFINITION	Gene encoding caffeine synthetase system-related enzyme and utilization thereof.		PART 31-JAN-2002
ACCESSION:	BD004679	GI:18632640		
VERSION	UP 2001037490-A/2.			
KEYWORDS	Camellia sinensis			
SOURCE	Camellia sinensis			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Theaceae; Camellia			
REFERENCE	Mizuno,M., Ashihara,A., Mizuno,K. and Fujimura,T. Gene encoding caffeine synthetase system-related enzyme and utilization thereof Patent: JP 2001037490-A 2 13-FEB-2001;			
AUTHORS	TITLE			
JOURNAL	COMMENT			
	OS Camellia sinensis			
	NCBI CHEM INC			
	PN JP 2001037490-A/2			
	PD 13-FEB-2001			
	PR 23-MAY-2000 JP 2000151718			
	PI MISANO MIZUNO AKIRA ASHIHARA KOICHI MIZUNO TATSUO FUJIMURA PO			
	C12N5/10, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, FC			
	C12N5/21, C12N9/10			
	PC C12P17/08, C12P23/00//C12N1/21, C12R1:19), (C12N5/10, C12R1:91),			
	FC C12N15/00,			
	PC C12N5/00, C12N5/90, C12N5/00, C12R1:91)			
	CC			
	FH Key			
	FT source			
	FT Location/Qualifiers			
FEATURES	source			
	Location/Qualifiers			
	1..1427			
	/organism="Camellia sinensis"			
	/db_xref="taxon:4442"			
BASE COUNT	444 a 251 c 330 g 402 t			
ORIGIN				
Query Match	10.7%; Score 138.8; DB 6; Length 1427;			
Best Local Similarity	51.8%; Pred. No. 37/e-25;			
Matches 461; Conservative 0; Mismatches 392; Indels 37; Gaps 5;				
QY 34	gagggcccaagaagtcctgcataatgatgaagaagtgaaggacatacgaactagccaagaa	93		
DB 80	GAAAGTGCAACGAAGGTGTTCATGAAACAGGGGGGAGAAGAAAGTAATATGACAAAAA	139		
OY 94	tgcattccacaatctcgctcttc--caagtggaaccttctcttagaacatgatatga	151		
DB 140	CTCTTCTTTACGCAACAAGTGGCTCAAATGGCACACGCCGTGAAAATGCAATTGA	199		
OY 152	gaattgttgvgggccaacttgcgcccaaatcaaaaagatgacatlaaagtctgggaattgga	211		
DB 200	AACCTCTTCTCCAGAGATTTCC-----ACCTTCAAGCTCTTACCGCAGAGACTGGGT	254		
OY 212	tgcgctttcgacaacaacacitttaacagtgcggagcatitgtgcaaatatgacaaa	271		
DB 255	TGTGACGCGGGTCCAACACTTCGCGATGATTTCTACGATCAAGAAATGATAAG	314		
OY 272	gttgcccaagaaagaagaatgaaatagaagctccaccacatcttatcttcgaatgat	331		
DB 315	AAATGAGGGAATTGA-----ATTCGCAAAACATGGAATCTCAAGGTTACTTGAAATAT	368		
OY 332	ccttccaaaatgatctcaattcgatttcgaagtgttcgaccaagtcttaaccgcaaatc	391		
DB 369	CTTTTGGAAATGATTTCAATACCCTTTCAAGGCGCTGTGCTGTAG-----	416		

[illegible]

Query Match	Best Local Similarity	Score	DB	Length
Matches 546; Conservative 0; Mismatches 482; Indels 72; Gaps 5;	49.6%;	134.8;	8;	1363;
59	aatgaagtgtagagcgatgacacgctacgacgaagatgcatccacatctggtctggc	118		
52	atggcagcgagatggtgaaatgactgcgcaacaaatctgcgcctgcaaaaattatgatg	111		
119	aagtgtaaaccttctcttgacacatgcatagagaattgtgtggcgcaactgccaac	178		
112	tcaaatcatgcatgatttttagacgaacaccccttaagatattatgcgtatcatggtggc	171		
179	atcaaaagtgtatgaagcttgtaggatttggaagcgctcttgaccacaaacaccttta	238		
172	ttcccaaaatgcttcaagatgcatgcatgattggtttgttcattcagagcgctaacccctttg	231		
239	acagtgtaggaatgtgcaagatgtgcaagatgtggccaagaaagagaatgaattta	238		
232	gtcatgtccgcgcatatttaattcaatttgagattt---gtacacaaagaaattttat	288		
299	gaacgtccacacatcagattttcttgaaatgattctttccaaaatgaattcaattcgat	358		
289	gaatttaccgattttgagatttttgcgaacgattcttcacgacacacatttcaaaccttc	348		
359	tccaagtctgcgaagctctacgcgaacatcgagaagaataatgacgaagataga	418		
349	ttcgaattgtttatc-----acatagaaatgga	375		
419	tcgtgcctaataagcgcaatgctctcttcttctacgagcagacttcccgagagatgc	478		
376	aactgcttggatgtattgatttgcctcgatctttctacggagacattatgctcaaaaaagac	435		
479	atgcatttttgacactctgttcaagtgctcatggtatctcaagttcccgaggttg	538		
436	cttacttttgcttattcttcttcaagatttactgctgctctcaggtcttgaagcgtg	495		
539	gtgattggaattgggattctggtgcaacaaaggagattatcctctccaaagatgtgt	598		
496	gaagattat-----aacacacaaacattttacatgacgaacgaaaggtct	540		
599	icgcgcgctccagaagcatatttgatcaatttgaagaagaatttccacatttctaag	658		
541	ccggaagtgtacaaacgatttcgcaaaagcaattcgaaacagcttctccacatttttaag	600		
659	atccattcgaagaagtgatttctacgtggcgaaatgctccctccacctgcatattgtaagta	718		
601	ttgcgagcgaggaattatgtaccagctggaacccatgcttgacatttttaacggcgaagt	660		
719	gagtaa-----ttgcgcgaacgaaatcccccagacttaacttgaacttgacata	766		
661	gttgaagaatccctgcgaacaaagatgactttatgcaattttcacttgcgttcgcaaaaacata	720		
767	aagacttattgttgaggagactctggagggaagaagaattgatttcaattcatca	826		
721	gtttatattgtgctgtagggcttgcacaaatgacgaatttgatctgctttacatttct	780		
827	ttcttcaacttcagcagaagaagaatgcatagttgagagaagaagttctcttgaa	886		
761	atttacttaccattgacccgcaagatgtagcgaacgaatttgcactgaactgaaggtctttacg	840		

Query Match 8.4% Score 108.4 DB 8 Length 1306



```
OY 737 aatcccttagacttactgtac-----atggcaataacgacttgattgttag 785
DB 761 CTGAATGCGTGTCTCATTTGGCAACTCTAGCCATGGCTCTCAATCAGATGGTTCTGAGG 820
OY 786 gacttcgtgagagagaaataatgatagtttcaataatccattcttaacctcagcag 845
DB 821 GACTAATAGAAAGAGAGAGATGATTAAGTTCAACATTCCTCAGATACACCATCTCCAA 880
OY 846 aagaagtaagtcatagttgagagagaggtctctgcgaatttataatctgagactt 905
DB 881 CAGAACTAGAACAGAGATCTTAAGAAAGGGCTTTTGTGATGACCATATAGAGGCTT 940
OY 906 ttaaggcccatatgatctgctctctctatgatgatattaccagtaagatcccatg 965
DB 941 CAGAAATATACTGGAGT-----AGCTGCACCTAAAGATGCTGATGGTGGCTGTTG 994
OY 966 aacaattaaagcagagatgtgcatcatttaattagatccagtttaagaaccatctcg 1025
DB 995 AGGAA---GAAGTTTACAGAGTGGCTGGTGGCATGAGACAGTGGCCGAGCATTTGCTGC 1051
OY 1026 caagtcatttggagagagctatataatgacttattcaagacttgcgaagcagcag 1085
DB 1052 TCGACCATTTTGTGTAAGCCATTCATGAAAGTGTGTTCCATAGGATTAACCTACATTA 1111
OY 1086 caaagttctccatcgtgcaagagctgctataataatctatcatctctctgcga 1145
DB 1112 TCGAAAGAAATGCTAAAGAGAGACCAAAATCATCAACGTCATGTCTCTCATTCGAA 1171
OY 1146 agccagagaagt 1157
DB 1172 AATCAGATTAAAT 1183
```

Search completed: July 27, 2002, 04:39:42  
Job time: 4583 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2002, 03:26:19 ; Search time 54.13 seconds  
(Without alignments)  
5890.122 Million cell updates/sec

Title: US-09-971-020-2

Perfect score: 1298  
Sequence: 1 agcagcgcgaatcgtatgt.....ataaaaaaaaaaaaaa 1298

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, NA: \*  
1: /cgn2\_6/ptodata/2/1na/5a.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/1na/5b.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/1na/5c.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/5d.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/5e.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/5f.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	3.2	1299	US-08-785-076-1	Sequence 1, Appl
2	39.8	3.1	3839	US-09-056-105-14	Sequence 14, Appl
3	38.2	2.9	991	US-08-924-747-25	Sequence 25, Appl
4	38.2	2.9	991	US-09-247-3738-25	Sequence 25, Appl
5	37.2	2.9	991	US-09-296-715-25	Sequence 25, Appl
6	36.6	2.8	120	US-07-867-106-2	Sequence 2, Appl
7	36.6	2.8	120	US-08-153-0518-28	Sequence 28, Appl
8	36.6	2.8	120	US-08-060-952C-44	Sequence 44, Appl
9	36.6	2.8	120	US-08-151-477A-28	Sequence 28, Appl
10	36.6	2.8	120	US-08-819-867-58	Sequence 58, Appl
11	35.8	2.8	1316	US-09-517-039-88	Sequence 88, Appl
12	35.8	2.8	1316	US-09-517-039-88	Sequence 88, Appl
13	35.2	2.7	3205	US-09-081-768A-3	Sequence 16, Appl
14	35	2.7	198	US-08-330-108-16	Sequence 16, Appl
15	35	2.7	198	PCT-US92-10087-16	Sequence 16, Appl
16	34.8	2.7	1915	US-09-120-365-2	Sequence 2, Appl
17	34.8	2.7	1915	US-09-515-039-2	Sequence 2, Appl
18	34.6	2.7	2238	US-08-617-8608-28	Sequence 28, Appl
19	34.6	2.7	2621	US-08-553-6198-8	Sequence 8, Appl
20	34.4	2.7	1174	US-07-869-933-10	Sequence 10, Appl
21	34.4	2.7	1174	US-09-103-663-10	Sequence 10, Appl
22	34.4	2.7	1446	US-08-596-024-5	Sequence 5, Appl
23	34.4	2.7	1446	US-09-020-818-5	Sequence 5, Appl
24	34.4	2.7	1446	US-08-907-740-5	Sequence 5, Appl
25	34.4	2.7	2334	US-08-062-632-4	Sequence 4, Appl
26	34.2	2.6	1089	US-09-004-731-15	Sequence 15, Appl
27	34.2	2.6	1089	US-09-004-731-17	Sequence 17, Appl

28	34.2	2.6	1089	US-08-749-699-15	Sequence 15, Appl
29	34.2	2.6	1089	US-08-749-699-17	Sequence 17, Appl
30	34.2	2.6	2606	US-08-408-318-1	Sequence 1, Appl
31	33.8	2.6	2606	US-08-839-164-1	Sequence 1, Appl
32	33.8	2.6	944	US-08-522-421-2	Sequence 2, Appl
33	33.8	2.6	1454	US-08-713-000-7	Sequence 7, Appl
34	33.8	2.6	1454	US-08-975-316-7	Sequence 7, Appl
35	33.8	2.6	1454	US-09-211-710-7	Sequence 7, Appl
36	33.8	2.6	1474	US-08-975-316-7	Sequence 7, Appl
37	33.8	2.6	3501	US-07-977-451-3	Sequence 3, Appl
38	33.8	2.6	3501	US-08-252-517-3	Sequence 3, Appl
39	33.8	2.6	3501	US-07-906-397A-3	Sequence 3, Appl
40	33.8	2.6	3501	US-08-601-891-3	Sequence 3, Appl
41	33.8	2.6	3501	US-09-021-324-3	Sequence 3, Appl
42	33.8	2.6	3501	PCT-US92-05401-3	Sequence 3, Appl
43	33.6	2.6	3501	PCT-US92-09893-3	Sequence 3, Appl
44	33.6	2.6	575	US-08-554-659-11	Sequence 11, Appl
45	33.6	2.6	1166	PCT-US96-12129B-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-785-076-1  
Sequence 1, Application US/08785076  
Patent No. 5789217  
GENERAL INFORMATION:  
APPLICANT: Hodgson, John  
TITLE OF INVENTION: NO. 5789217el tRNA Synthetase  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/785,076  
FILING DATE: 17-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION NUMBER: 9601096.2  
APPLICATION NUMBER: 961845.6  
FILING DATE: 19-JAN-1996  
APPLICATION NUMBER: 961845.6  
FILING DATE: 27-JUL-1996  
APPLICATION NUMBER: 9622617.0  
FILING DATE: 30-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmil, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P1334-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1299 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-785-076-1



RESULT 3  
 US-08-924-747-25  
 Sequence 25 Application US/08924747  
 Patent No. 6063570  
 GENERAL INFORMATION:  
 APPLICANT: MCGONIGLE, BRIAN  
 APPLICANT: O'KEEFE, DANIEL  
 TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE  
 TITLE OF INVENTION: ENZYMES  
 NUMBER OF SPOUNCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY

;  
;  
;  
US-08-924-747-25

Db . 959 AAAAAAAAAA 969

```

; TYPE: DNA
; ORGANISM: SOYBEAN

```

Query Match	2.9%	Score 38.2;	DB 4;	Length 991;
Best Local Similarity	55.7%	Pred. No. 0.26;		
Matches	73;	Conservative	0;	Mismatches 58;
			Indels	0;
			Gaps	0;

07 1177 <https://doi.org/10.1016/j.ccr.2017.05.001> Best Local Similarity Matches 69; Conservative 0; Mismatches 53; Indels 0; Gaps 0



```

RESULT 9
US-08-151-477A-28
Sequence 28, Application US/08151477A
Patent No. 5830644

GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woe Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott A. Weirich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: Storage File
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FAST-SEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,477A
FILING DATE: NO. 5830644ember 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Waidburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 9489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 120
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
US-08-151-477A-28

Query Match 2.88; Score 36.6; DB 2; Length 120;
Best Local Similarity 71.6%; Pred. No. 0.3; Mismatches 19; Indels 0; Gaps 0;
Matches 48; Conservative 0;

OY 1232 gcaataaagatgagtcgaagaaataagatattagttacacatttcctataaataaaaaa 1291
Db 30 GGAATTACTTGCAATGAGAGAAATTAATAACATTTGGCACCTGTGTAATAAATAAAAAA 89

OY 1292 aaaaaa 1298
Db 90 AAAAAA 96

RESULT 10
US-08-819-867-58
Sequence 58, Application US/08819867
Patent No. 6007989

```

```

GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Jerry Shay
APPLICANT: Woodling E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon S. Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
ZIP: 90071-5065
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSO for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819, 867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/153, 051
FILING DATE: NO. 6007989ember 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chanels Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/2232
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-58

Query Match: 2.88; Score 36.6; DB 3; Length 120;
Best Local Similarity 71.6%; Pred. No. 0.3; Indels 0; Gaps
Matches 48; Conservative 0; Mismatches 19;

QY 1232 gtaataaagtgatgtgcaagataagataatttgtagcaaatatttcataaaaaaaaaa 1299
Db 30 GTAATAACTTGCAATGTGAGAGATAAACAATTGTGGCACTTGTGTAATAAAAAAAAAAAAAA 89
Db 1292 aaaaaaa 1298
Db 90 AAAAAAA 96

RESULT 11
US-09-120-365-88
Sequence 88, Application US/09120365
Patent No. 6103514

```

```

: GENERAL INFORMATION:
: APPLICANT: Natori, Shunji
: TITLE OF INVENTION: NEW PROTEASE
: FILE REFERENCE: 32290-144749
: CURRENT APPLICATION NUMBER: US/09/120,365
: CURRENT FILING DATE: 1998-07-22
: EARLIER APPLICATION NUMBER: JP 9-333 474
: EARLIER FILING DATE: 1997-11-18
: NUMBER OF SEQ ID NOS: 101
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 88
: LENGTH: 1916
: TYPE: DNA
: ORGANISM: Sarcophaga peregrina
: US-09-120-365-88

Query Match          2.8%; Score 35.8; DB 3; Length 1916;
Best Local Similarity 53.6%; Pred. No. 1.6;
Matches 96; Conservative 0; Mismatches 82; Indels 1; Gaps 1;

QY 1116 ataatacttcatctctcgcgaagaagccagagagcagcagcgtgtgaaagtgtg 1175
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1739 ataattgctgtttagtcacatgcccactatgtagagatgacataattgtatgtcgtg 1798
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1176 ttcttagtggttttggcgggtgggtgttgcgggtatgttgcgtttgtatcgttaa 1235
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1799 cttaagagcttataaaagacttaatttcatttaatttccttcaattttttttta 1858
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1236 taaaagtgtgcaagaataagatattagtacaattttccttaaaaaa 1294
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1859 t-aagttgtctactcaataataagaataataaattgttttaatacaaaaaa 1916
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13

```

```

: US-09-061-768A-3
: Sequence 3, Application US/09061768A
: Patent No. 620437
: GENERAL INFORMATION:
: APPLICANT: BRASH, ALAN R.
: APPLICANT: BOEGLIN, WILLIAM E.
: APPLICANT: JISAKA, MITSUO
: TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ARLES A. TAYLOR, JR.
: STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
: CITY: DURHAM
: STATE: NORTH CAROLINA
: COUNTRY: USA
: ZIP: 27707
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
: COMPUTER: IBM PC/XT/AT compatible
: OPERATING SYSTEM: Windows 3.1
: SOFTWARE: WORD PERFECT 6.1 and ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/061,768A
: FILING DATE: APRIL 16, 1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA: NONE
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: ARLES A. TAYLOR, JR.
: REGISTRATION NUMBER: 39,395
: REFERENCE/DOCKET NUMBER: 1242/5
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 493-8000
: TELEFAX: (919) 419-0383
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3205 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: US-09-061-768A-3

Query Match          2.7%; Score 35.2; DB 4; Length 3205;
Best Local Similarity 52.8%; Pred. No. 2.8;
Matches 76; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1155 agtcaagcgtgtaaaagtttttttagttgttttggcgttggtgggtcttcggt 1214
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 3061 agtttgcgtgtagagcgtttttttttgtttgtttgctttgttggctttgttttgg 3120
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1215 attgtcgtttgtattcgttaataaagtgatgcaagaataagatatattgtacatat 1274
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 3121 tttttgattttgtttttctgttcgcttcacactgcacgttcatttaattgcatatga 3180
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1275 ttctataaaaaa 1298
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 3181 gttcatttcacaaaaa 3204
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
: US-08-330-108-16
: Sequence 16, Application US/08330108
: Patent No. 5795752
: GENERAL INFORMATION:
: APPLICANT: Smith, Kendall A.
: TITLE OF INVENTION: IL-2-Stimulated Gene
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lathive & Cockfield

```

```

STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,108
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,736
FILING DATE:
APPLICATION NUMBER: US/07/796,066
FILING DATE:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single stranded
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
CELL TYPE: T-cell blast
IMMEDIATE SOURCE:
LIBRARY:
CLONE: BD4-T3
US-08-330-108-16

Query Match          2.7%; Score 35; DB 1; Length 198;
Best Local Similarity 55.3%; Pred. No. 1;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

OY 1176 tttttagtggttttgccgttgagggtcttcggtatctgcttgcgtatcgttaa 1235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 52 ttttcttttccgtttttatttttttgaagtcgttgcctttatttgaagctgtta 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1236 taaaagtgtatgcaagaataagatattagcacatatttcataaaaaaaaaa 1295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 112 TAAATATATATATATATATATATATATATATATATATATATATATATAT 171
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1296 aaa 1298
    |||
DB 172 AAA 174

```

```

SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10087
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA: 07/796,066
APPLICATION NUMBER: 07/796,066
FILING DATE: 20-NOVEMBER-1991
ATTORNEY/AGENT INFORMATION:
NAME: DeConfil, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-028PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
TELEFAX: 617-227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
CELL TYPE: T-cell blast
IMMEDIATE SOURCE:
LIBRARY:
CLONE: BD4-T3
PCT-US92-10087-16

Query Match          2.7%; Score 35; DB 5; Length 198;
Best Local Similarity 55.3%; Pred. No. 1;
Matches 68; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

OY 1176 tttttagtggttttgccgttgagggtcttcggtatctgcttgcgtatcgttaa 1235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 52 ttttcttttccgtttttatttttttgaagtcgttgcctttatttgaagctgtta 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1236 taaaagtgtatgcaagaataagatattagcacatatttcataaaaaaaaaa 1295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 112 TAAATATATATATATATATATATATATATATATATATATATATATATAT 171
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 1296 aaa 1298
    |||
DB 172 AAA 174

```

Search completed: July 27, 2002, 04:40:45  
 Job time: 4466 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2002, 03:21:59 / Search time 1730.1 Seconds  
(without alignments)  
10126.032 Million cell updates/sec

Title: US-09-971-020-2

Sequence: 1 agcagcgcgcacatcgcattgtc.....ataaaaaaaaaaaaaaaaaa 1296

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estro:\*  
7: em\_estro:\*  
8: em\_estro:\*  
9: em\_estro:\*  
10: em\_estro:\*  
11: em\_estro:\*  
12: em\_estro:\*  
13: em\_estro:\*  
14: em\_estro:\*  
15: em\_estro:\*  
16: em\_estro:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198.8	15.3	848	10	BS586603 EST488371
2	161.8	12.5	676	10	BS586603 EST488371
3	146.2	11.3	542	9	BE202402 EST192551
4	145.6	11.2	637	10	BE2004424
5	145	11.2	495	9	AL368351
6	136.2	10.5	604	10	BE0004423
7	129	9.9	539	10	BE645937
8	129	9.9	685	9	AM774361
9	127	9.7	716	10	BS585368
10	125	9.6	711	10	BE202392
11	125	9.6	474	9	BE202392
12	117.2	9.0	723	10	BS585571
13	109.8	8.5	482	10	BS205540
14	108.2	8.3	678	10	BS120946
15	107.8	8.3	455	10	BS156251
16	107.8	8.3	500	10	BS156251
17	107.8	8.3	500	10	BS156251

18	106.2	8.2	637	9	AM217769
19	106	8.2	451	9	AL369180
20	104.6	8.1	466	10	BS586994
21	104.6	8.1	481	10	BS789602
22	104.2	8.0	451	10	BS044410
23	104.2	8.0	495	10	BS045001
24	104	8.0	445	10	BE009759
25	104	8.0	535	9	AM735668
26	104	8.0	568	9	AM584129
27	103.6	8.0	466	10	BS042646
28	103.2	8.0	434	10	BS586091
29	102.6	7.9	483	10	BS790118
30	102.2	7.9	561	9	AM217770
31	102.2	7.9	561	9	AM228332
32	102.2	7.9	611	9	AM622895
33	102.2	7.9	611	9	AM928688
34	102.2	7.9	611	10	BS1930765
35	101.8	7.8	568	10	BS1927279
36	100.8	7.8	702	10	BM301977
37	98.8	7.5	773	10	BM413186
38	97.6	7.5	698	10	BS669572
39	93.8	7.2	503	10	BS192552
40	92.8	7.1	588	10	BS097739
41	92.2	7.1	545	9	AM928283
42	91.4	7.0	584	9	BE205019
43	90.2	6.9	561	10	BE462469
44	89.8	6.9	561	10	BE358619
45	88.8	6.8	578	10	BE359581

## ALIGNMENTS

RESULT 1  
LOCUS BS586603  
DEFINITION BS586603 MHAM Medicago truncatula/Glommus versiforme mixed EST  
ACCESSION BS586603  
VERSION BS586603.1 GI:13601667  
KEYWORDS EST  
SOURCE Medicago truncatula/Glommus versiforme mixed EST library  
ORGANISM Medicago truncatula/Glommus versiforme mixed EST library  
REFERENCE 1 (bases 1 to 848)  
AUTHORS Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.  
and Fraser,C.M.  
TITLE ESTs from roots of Medicago truncatula after colonization with  
Glommus versiforme, 2001  
JOURNAL Unpublished (2001)  
COMMENT Contact: Harrison M.J.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401  
Tel: 580-223-5810  
Fax: 580-221-7380  
Email: mjharrison@noble.org  
Noble EST name: N385669e TIGR sequence name: MTDCUL17k More  
information is available at: <http://www.medicago.org>  
Seq primer: 5' end (CTA gaa gta gta CC).  
Location/Qualifiers  
1. 848  
/organism="Medicago truncatula/Glommus versiforme mixed EST  
library"  
/cultivar="Medicago truncatula genotype A17"  
/db\_xref="taxon:115092"  
/clone="pMRAM-44A21"  
/clone\_id="MRAM"  
/tissue-type="roots colonized with Glommus versiforme"  
/dev-stage="Roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glommus versiforme. The library was  
made from a mixture of RNA from each of these stages."  
/lab\_host="E. coli strain XL0LR"



/note="Vector: pBluescript SK<sup>+</sup> Site-1: EcoRI; Site-2: XhoI; cDNA was prepared from polyA<sup>+</sup> enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with *Glomus versiforme*. The cDNA was directionally ligated into the Uni-Zap XR vector from *Stratagene* and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in *XIOLR* cells."

BASE COUNT 259 a 166 c 165 g 258 t

Query Match 15.3% Score 198.8; DB 10; Length 848;  
Best Local Similarity 57.7%; Pred. No. 1.5e-27;  
Matches 422; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

OY 13 tgcattgtctctcatatgaatgagctccaaagaatcgtcatatgaatgagtgagg 72  
DB 60 tccatgacgacccctttgacaaatgagcttgaaacaaagcttccatgaatgagtgagg 119  
OY 73 cgaataagctacgcaagaatgacatcct--acaatcgtgctcttgccaagtgaacc 129  
DB 120 agatgacaaacgttgcamaatactccacatttcagaaatgctgagctgacggcaaaaca 179  
OY 130 ttctcttgcacatgacacagagaatgtgtcgcgccaaacttgcacacacacaaagt 189  
DB 180 tatgactgaaagagatgataatgagctgattgtgacacttttccaat-----tg 230  
OY 190 catlaaagctgagattgagtgagcttctgcacacacacacatttaacagtgaggg 249  
DB 231 ttgtaagagctgacgttaggtgtgtcatcagctccaaatgacatttggtagatcama 290  
OY 250 catgagcaaatgattgacaaagtgcgaggaagaatgagatgaagaagctccac 309  
DB 291 tatcaataaacatattgactgtgagctcaaaattgagctatgagctca-----ccca 344  
OY 310 catcagattttctgagatgactctttccaaatgattcaatcgtgttcaagtgtct 369  
DB 345 gtttcagattttctgagatgactctttccaaatgattcaatcgtgttcaagtgtct 404  
OY 370 gccaaagcttctacgcaaaactcgagaagaataatgagcagaatgagtgagctaat 429  
DB 405 accctgattttatataaaacacacacacacacacacacacacacacacacacacac 464  
OY 430 aagcgaatgctgagctcttcttcaagcagaactcttcccgagagagctcattttt 489  
DB 465 taatgacaaacacctgagcttcttcaagcagaactcttcccgagagagctcattttt 524  
OY 490 gcaactcttctacagtgatgattcagtgatgagtgagtgagtgagtgagtgagtg 549  
DB 525 tcatctcctcctatgactgacacacacacacacacacacacacacacacacacacac 584  
OY 550 gggagatggtgacaaagaagagatatttaccctccaaagaatgagtgagtgagtgag 609  
DB 585 tatgacaaacacacacacacacacacacacacacacacacacacacacacacacac 644  
OY 610 gaagcgaatgagtgacacacacacacacacacacacacacacacacacacacacac 669  
DB 645 aaaaacacacacacacacacacacacacacacacacacacacacacacacacacac 704  
OY 670 agagtggttttcaagtgagcgaatgagtgagtgagtgagtgagtgagtgagtgag 729  
DB 705 tgaactgcttctcctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 764  
OY 730 cgaacgaatcc 741  
DB 765 acttatgacatgc 776

RESULT 2  
BI2171770 BI2171770 676 bp mRNA linear EST 18-JUL-2001  
LOCUS

DEFINITION NF011D12FL1101 Developing flower *Medicago truncatula* cDNA clone  
NF011D12FL 5', mRNA sequence.  
BI2171770  
VERSION  
BI2171770.1 GI:14880529  
KEYWORDS  
EST.  
SOURCE  
ORGANISM  
Medicago truncatula  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.

REFERENCE 1 (bases 1 to 676):

AUTHORS

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, C.J.,

Flores, H.R., Iman, J.T., Weller, J.W., and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula flower library

Unpublished (2001)

CONTACT: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7391

Fax: 580 221 7380

Email: gdmay@noble.org

Insert Length: 676 Std Error: 0.00

Plate: 011 row: D column: 12

Seq primer: TCACACAGGAACACCTATGAC.

Location/Qualifiers

1. 676

/organism="Medicago truncatula"

/db\_xref="taxon:3880"

/clone="NF011D12FL"

/clone\_lib="developing flower"

/tissue\_type="developing flowers"

/dev\_stage="developmentally pooled. Contains a mixture of

very young, developing, fully-opened flowers and flowers

in early transition into pods."

/note="Vector: Lambda Zap; cDNA was prepared from polyA+

enriched, pooled samples of equivalent amounts of total

RNA from very young, developing, fully-opened flowers and

flowers transitioning into pods. The cDNA was

directionally ligated into the Uni-Zap XR vector

(Stratagene) and packaged using the GigaPack III Gold

packaging extracts. Phagemids containing cDNA inserts were

in vivo excised from the recombinant Uni-Zap XR vector

using Ex-assist helper phage and the E. coli strain

XI1-Blue MRF<sup>+</sup> (Stratagene). Excised plasmids were plated

using SOLR cells."

BASE COUNT 232 a 124 c 126 g 191 t 3 others

ORIGIN

Query Match 12.5% Score 161.8; DB 10; Length 676;  
Best Local Similarity 57.1%; Pred. No. 1.3e-20;  
Matches 333; Conservative 0; Mismatches 244; Indels 6; Gaps 2;

OY 299 gaagctccacacacacacacacacacacacacacacacacacacacacacacacacac 358  
DB 64 gacgacacacacacacacacacacacacacacacacacacacacacacacacacacacac 123  
OY 339 ttcaagtgctgctgcaagctcttaccgcaaacctcgagaagaagaatgagcagaatagaga 418  
DB 124 ttgaaagttagctacacacacacacacacacacacacacacacacacacacacacacac 183  
OY 419 tcgagcctaagaagcgaatgctcttcttcaagcagagacacacacacacacacacacacac 478  
DB 184 ccattgcttcaatgaaacacacacacacacacacacacacacacacacacacacacacac 243  
OY 479 atgacatttttgacacacacacacacacacacacacacacacacacacacacacacacac 538  
DB 244 atagatttttttgcattcttctgctgctgctgctgctgctgctgctgctgctgctgctg 303  
OY 539 gtgattgaattgggagtggtgcaacaagaagatattacacacacacacacacacacacac 598





OY 485 ttittgactctgtttacagtglttcatgttgatcctcaggttccagcggttgatgt 544  
 DB 347 TTTTATTCCTCCCTATGCTCTACAGCTGCTTCCAAAGATCCATGATTCAGAGAT 406  
 OY 545 gaattggagatgtgtgcaacaagaaggagatttacccttccaaaggagtcgcagcc 604  
 DB 407 GCTGCTATTAACCAATTGATCAAGGAATATTACTTAACAAGACCAAGCCCTCAGCA 466  
 OY 605 gtccagaagcattatgttgatcattt 631  
 DB 467 GTGCAAAAACATACCTTTGACAAATTT 493  
 RESULT 6  
 BE004423  
 LOCUS EST432921 kV1 Medicago truncatula cDNA clone pKV1-17L3, mRNA  
 DEFINITION  
 ACCESSION BE004423  
 VERSION BE004423.1 GI:10704698  
 KEYWORDS  
 SOURCE EST  
 ORGANISM  
 barrel medic.  
 Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 1 (bases 1 to 604)  
 VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,  
 Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and  
 Fraser, C.M.  
 ESTs from roots of Medicago truncatula 24 hours after inoculation  
 with Sinorhizobium meliloti  
 Unpublished (1999)  
 JOURNAL  
 COMMENT  
 CONTACT: VandenBosch K  
 Department of Biology  
 Texas A&M University  
 College Station, TX 77843-3258, USA  
 Tel: 409 845 7707  
 Fax: 409 845 2891  
 Email: Kate@mail.bio.tamu.edu  
 Texas A&M University name: T268233e TIGR sequence name: MT1BE62TK  
 More information is available at: http://chryslr.tamu.edu/medicago  
 Seq primer: SKmod (CTA gaa cta gta gat cc).  
 Location/Qualifiers  
 1..604  
 /organism="Medicago truncatula"  
 /cultivar="genotype A17"  
 /db\_xref="taxon:3880"  
 /clone="pKV1-17L3"  
 /clone.lib="KV1"  
 /tissue-type="Seedling roots"  
 /dev\_stage="24 hours post-inoculation with Sinorhizobium  
 meliloti"  
 /lab\_host="E. coli strain XLOLR"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA  
 was directionally ligated into the Unipap XR vector from  
 StrataGene and packaged using Gigapack III Gold packaging  
 extracts. Plasmids containing cDNA inserts were excised  
 from the recombinant lambda-zap phage using Ex-assist  
 helper phage and propagated in XLOLR cells."  
 BASE COUNT 197 a 104 c 143 g 160 t  
 ORIGIN  
 Query Match 10.5%; Score 136.2; DB 10; Length 604;  
 Best local Similarity 55.3%; Pred. No. 8.1e-16;  
 Matches 264; Conservative 0; Mismatches 213; Indels 0; Gaps 0;  
 OY 563 aacacaggagatcttacccttccaaaggatgtgcgcgcgcgaaggagcatttg 622  
 DB 128 AACAAAGGATATTATTCCTACACAGACAGCCCTCCAGCAGTGCAAAAAACATCTTT 187

OY 623 gatcaattcagaagaatttaccacatttccaaagattcagaagatgtgttca 682  
 DB 188 GAACAATTTTCAACAAGATTTTCTCATTTTAAAGATACGTTCTGTGAACGCTTCT 247  
 OY 683 cgtggcgaatgtctcttacccttgatcttgtaaaagatgaaatcgcaaacgaatccc 742  
 DB 248 AGTGTGCGCATGCTGCTTAACCTATTATGGCAGAGATGACCAAAATGAACTTATGAAGCA 307  
 OY 743 ctgaacttctgacatgcaataaagcattgtattgtgaggaacttggaggaagaa 802  
 DB 308 TGGGTGTATTGGCATGCGACATGATGATGCGCCAGTGAATGTGTAGAGCAATCA 367  
 OY 803 aaattgataatttcaatcatttccatttccacttcagcagaagaagtatgata 862  
 DB 368 AANTGACATCTTAAACATACATCCTATTGGCCTGATGAGATATGAAAGTG 427  
 OY 863 gtgagagagaagtgcttgcgaatttatatcgtgaacttgaagcccatatgat 922  
 DB 428 ATTGAAGAAAGAGGCTCTTTGATGTTCAAGGTTAGACAAATTAAGACGATTTGGCTG 487  
 OY 923 gctgcttctctatgataatgataatccagtaagatcccaatgaacaaatgaagcag 982  
 DB 488 AAAACGCTGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547  
 OY 983 tatgtgcatcattatgaatgaatcagtttaagacccatccctgcagatcatttga 1039  
 DB 548 GGTGTGACAAAGTTTATTAAGAGCTGTGACGAACCAATTTTGAAGTCAGAGTTTGA 604  
 RESULT 7  
 BE645937/c  
 LOCUS ESM507556 kV3 Medicago truncatula cDNA clone pKV3-48C3 5' end, mRNA  
 DEFINITION  
 ACCESSION BE645937  
 VERSION BE645937.1 GI:13781049  
 KEYWORDS  
 SOURCE EST  
 ORGANISM  
 barrel medic.  
 Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 1 (bases 1 to 539)  
 VandenBosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D., Bowman,  
 C.L., Craven, M.B., Cho, J., and Fraser, C.M.  
 ESTs from roots of Medicago truncatula 72 h after Rhizobium  
 inoculation, 2001  
 Unpublished (2001)  
 JOURNAL  
 COMMENT  
 CONTACT: VandenBosch K  
 Department of Biology  
 Texas A&M University  
 College Station, TX 77843-3258, USA  
 Tel: 409 845 7707  
 Fax: 409 845 2891  
 Email: Kate@mail.bio.tamu.edu  
 M594344e TIGR sequence name: MTCE1141r More information is  
 available at: www.medicago.org  
 Seq primer: SKmod (CTA gaa cta gta gat cc).  
 Location/Qualifiers  
 1..539  
 /organism="Medicago truncatula"  
 /cultivar="genotype A17"  
 /db\_xref="taxon:3880"  
 /clone="pKV3-48C3"  
 /clone.lib="KV3"  
 /tissue-type="Seedling roots"  
 /dev\_stage="3 days post-inoculation with Sinorhizobium  
 meliloti"  
 /lab\_host="E. coli strain XLOLR"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA

was directionally ligated into the Unizap XR vector from  
stratagene and packaged using giga-pack III Gold packaging  
extracts. Plasmids containing CDNA inserts were excised  
from the recombinant lambda-zap phage using Ex-assist  
helper phage and propagated in XL04R cells."

BASE COUNT 159 a 128 c 76 g 176 t

Query Match 9.98; Score 129; DB 10; Length 539;  
Best Local Similarity 55.18; Pred. No. 1.9e-14;  
Matches 252; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

615 caatttgatcaatttcaagaagatttaccacatttcaaggaattcgaagaagt 674  
|||||  
Db 539 CAACTTGAACAATTTCAACAGATTTCTCATTTTAAAGATCAGCTGCTGAC 480  
675 tgtttcagctggccgaatgctcttaccctgcattgttaagtagaattcgaagaac 724  
|||||  
Db 479 TGCTTCCTAGTGTGCTGCTTAACTTATTTGGCAGAGATGACCAAAATGACTTA 420  
673 cgaatcccttagacttacttgaatgaataaagacttgaatgaatcttg 794  
|||||  
Db 419 TGAATGATGCTGTCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
675 aggaagaagaatggaatggttcaatatttaccatttaccattcagaagaagtaa 854  
|||||  
Db 359 AGCAATCAAAATTTGCTCATTTTACATTCACATCTTATTTGCTGCTGCTGCTG 300  
855 agtgcatagttgaagaagaaggtcttcggaatttatacttgaagaacttgaagccc 914  
|||||  
Db 299 GAAAGTGATTAAGAAAGAGGCTTTTGAATGATTTAAAGTTAAAGCAATTTGAACGG 240  
915 attatgctgctcctctctatattgaatgattaccagtaagaccatgaacaaatta 974  
|||||  
Db 239 ATTGGGTGAAAAACCTGATGATGATGATGATGATGATGATGATGATGATG 180  
975 aagcagaatattggaatcaatattatagatcagtttcaagaaccatctcgaagcatt 1034  
|||||  
Db 179 GGCTGAGGCTGTACCAAGATTATTAAGAGCTGTGCAACCAATTTGAAGTACAGT 120  
1035 ttggaagaagctatttgcctgacttaccacagagct 1071  
|||||  
Db 119 TTGGAGAAAGAAATATATGATGATGATGATGATGATGATGATGATGATG 83

RESULT 8  
AM774361/c 685 bp mRNA linear EST 07-SEP-2000  
LOCUS EST33512 KV3 Medicago truncatula cDNA clone PKV3-22618, mRNA  
DEFINITION sequence.  
ACCESSION AM774361  
VERSION AM774361.1 GI:7718276  
KEYWORDS EST.  
SOURCE  
ORGANISM  
barrel medic.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Vandenbosch, K., Hunt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,  
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and  
Fraser, C.M.  
ESTs from roots of Medicago truncatula after Rhizobium inoculation  
Unpublished (1999)  
Contact: Vandenbosch K  
Department of Biology  
Texas A&M University  
College Station, TX 77843-3258, USA  
Tel: 409 845 7707  
Fax: 409 845 2891  
Email: Kate@mail.bio.tamu.edu

Texas A&M EST name: T257780E  
TIGR sequence name: MREA457K  
More information is available at:  
<http://chrystle.tamu.edu/medicago>  
Seq primer: SKM04 (CTA GAA CTA gct gat CC).  
Location/Qualifiers

FEATURES  
source  
1. 685  
/organism="Medicago truncatula"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone="PKV3-22618"  
/clone\_1db="KV3"  
/tissue\_type="Seedling roots"  
/dev\_stage="3 days post-inoculation with Sinorhizobium  
meliloti"  
/lab\_host="E. coli strain XL04R"  
/note="Vector: pBluescript SK-; Site, 1: EcoRI; Site, 2:  
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA  
was directionally ligated into the Unizap XR vector from  
stratagene and packaged using giga-pack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-zap phage using Ex-assist  
helper phage and propagated in XL04R cells."

BASE COUNT 228 a 148 c 91 g 218 t

Query Match 9.98; Score 129; DB 9; Length 685;  
Best Local Similarity 55.18; Pred. No. 1.7e-14;  
Matches 252; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

615 caatttgatcaatttcaagaagatttaccacatttcaaggaattcgaagaagt 674  
|||||  
Db 685 CAACTTGAACAATTTCAACAGATTTCTCATTTTAAAGATCAGCTGCTGAC 626  
675 tgtttcagctggccgaatgctcttaccctgcattgttaagtagaattcgaagaac 734  
|||||  
Db 625 TGCTTCCTAGTGTGCTGCTTAACTTATTTGGCAGAGATGACCAAAATGACTTA 566  
735 cgaatcccttagacttacttgaatgaataaagacttgaatgaatcttg 794  
|||||  
Db 565 TGAATGATGCTGTCTCATTTTACATTCACATCTTATTTGCTGCTGCTGCTG 506  
795 aagcagaagaatggaatggttcaatatttaccatttaccattcagaagaagtaa 854  
|||||  
Db 505 AGCAATCAAAATTTGCTCATTTTACATTCACATCTTATTTGCTGCTGCTGCTG 446  
855 agtgcatagttgaagaagaaggtcttcggaatttatacttgaagaacttgaagccc 914  
|||||  
Db 445 GAAAGTGATTAAGAAAGAGGCTTTTGAATGATTTAAAGTTAAAGCAATTTGAACGG 386  
915 attatgctgctcctctctatattgaatgattaccagtaagaccatgaacaaatta 974  
|||||  
Db 385 ATTGGGTGAAAAACCTGATGATGATGATGATGATGATGATGATGATGATG 326  
975 aagcagaatattggaatcaatattatagatcagtttcaagaaccatctcgaagcatt 1034  
|||||  
Db 325 GGCTGAGGCTGTACCAAGATTATTAAGAGCTGTGCAACCAATTTGAAGTACAGT 266  
1035 ttggaagaagctatttgcctgacttaccacagagct 1071  
|||||  
Db 265 TTGGAGAAAGAAATATATGATGATGATGATGATGATGATGATGATGATG 229

RESULT 9  
AL371374/c 499 bp mRNA linear EST 03-AUG-2000  
LOCUS AL371374  
DEFINITION MREA45607R1 MREA Medicago truncatula cDNA clone MREA45607 T7, mRNA  
sequence.  
ACCESSION AL371374  
VERSION AL371374.1 GI:9671127  
KEYWORDS EST.  
SOURCE  
barrel medic.

	ORGANISM
	Medicago truncatula
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Rosidae; Fabales; Fabaceae; Papilionoideae; Trifolieae
	Medicago.
REFERENCE	1 (bases 1 to 499)
AUTHORS	Journet,E.P., Crespeau,H., van Tuinen,D., Guzy,J., Jallion,O., Mibel,A., Carreau,V., Chataigner,O., Kahn,D., Glaninazzi-Pearson ,V. and Gamas,P.
TITLE	Medicago truncatula ESTs from nitrogen-starved roots
JOURNAL	Unpublished (2000)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email : seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : Mt-est@toulouse.inra.fr Website : <a href="http://sequence.toulouse.inra.fr/Mtruncatula.html">http://sequence.toulouse.inra.fr/Mtruncatula.html</a> ).
FEATURES	Location/Qualifiers
source	1..499
	/organism="Medicago truncatula" /cultivar="Jemalong" /db_xref="taxon:3880" /clone="MCBA43C07" /clone_1fb="MTBA" /tissue_type="root tips" /dev_stage="harvested after 3 days of N-starvation" /note="Vector: pBluescript psk; Site1: EcoRI; Site2: XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into uni-zapR vector from stratagene and packaged using GibcoBRL Gold packaging extracts. plasmids containing cDNA inserts were mass-excisied from phage stock using exsaiit helper phage and propagated in SGR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."
BASE COUNT	168 a 96 c 88 g . 147 t
ORIGIN	
	Query Match 9.88; Score 127; DB 9; Length 499; Best Local Similarity 58.88; Pred. No. 4.5e-14; Matches 284; Conservative 0; Mismatches 180; Indels 19; Gaps 3
Db	13 tcgaattgcctgcatatgatgatgagtcacaaagaatcctgtcatatgatatgaagtgaagtgaag 72
Db	468 TCGTAGCTACCCCTTTAGCAATGGGACGAGTGAACAACGCCCTTGACATGTGAATGGAGTGAAGG 409
Db	73 cgatacaagctacgccaagaatg----cacctacaactctggcccttgccaagtgtgaac 128
Db	408 AGATTACACACTATGCAGATTAATCCACATTTTCACAGAATGATGATCTCACGCCAAAC 349
Db	129 ctcttcctgaaacaagcataagagatctftgcggccaacttgcaccaatcatacaagt 188
Db	348 ATTATCTGTGAAGAAGTATAATGAGCOTGATTATGTGACACTTTTCCAAT-----T 298
Db	189 gcatttaaatcttgcaattgttggaatcgctcttcggcgaacaaaacaccttttaacagtg 248
Db	297 GTTTGAAGTGGCTACTAGTTCGATCATACAGTCCAAAAGCACCCTTTTGATGATCAA 238
Db	249 acatttgcaagaattttgacaaagtctggccagaagaagaagaatgatgatgacgtccca 308
Db	237 ATATCATTAACACACTATATCTCTGTGATCAAAAAATGTGCTATGATGAC-----CCA 184
Db	309 ccattcaagattcttcgaagatcctttccaaaaatgatattcaattcaggctttccaagtgc 368
Db	183 TGTTTCAAGTTTTCTCCATATACCTATTATTGGAATGAGACTCAATATCACACTTTAAGATTAC 124

```

Yc 369  tgcgaagcttcaccgcgaacatcgagaaagaataatgagcgaagatgagatcgacctaa 428
Db 123  TACGCGATTTTATATAAAGACCTCAAGAAAGAGCAAAAGTTTATGTCACATGTTC 64
Yc 429  taagagcaatcgctgcgcgtcttcctcgcgaagacttcgccgagagatcatgatttt 488
Db 63  TTAGTGGAACACCTGGGTCTTTTATATGGAGACCTTCGCCGACAAATTCACATTT 4
Yc 489  tgc 491
Db 3  TTC 1

RESULT 10
BG585368
LOCUS
DEFINITION
EST487132 MHAM Medicago truncatula/Gloms versifforme mixed EST
Library CDNA clone pMHAM-22N19 5' end, mRNA sequence.
ACCESSION
BG585368
VERSION
BG585368.1 GI:13600432
KEYWORDS
EST.
ORGANISM
Medicago truncatula/Gloms versifforme mixed EST library.
SOURCE
Medicago truncatula/Gloms versifforme mixed EST library
Eukaryote; mixed EST libraries.
REFERENCE
1 (bases 1 to 716)
Harrison,M.J., Liu,T., Town,C.D., Van Aken,S., Utterback,T., Cho,J.T.
and Fraser,C.M.
ESTs from roots of Medicago truncatula after colonization with
Gloms versifforme, 2001
Unpublished (2001)
CONTACT: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation.
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7280
Email: mjharrison@noble.org
Noble EST name: N580842e TIGR sequence name: MTDCC82K More
information is available at: http://www.medicago.org
Seq primer: Skmcd (CTA GAA CTA gta gat CC).
FEATURES
Source
1. 716
/organism="Medicago truncatula/Gloms versifforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-22N19"
/clone_1ib="MHAM"
/tissue_type="Roots colonized with Gloms versifforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Gloms versifforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOIR"
/notice="Vector: Bluescript SK+. Site1: EcoRI; Site2:
XhoI. CDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Gloms versifforme. The cDNA was
directionally ligated into the Uniap XR vector from
stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-85s1st
helper phage and propagated in XLOIR cells."
BASE COUNT
238 a 114 c 167 g 197 t
ORIGIN
Query Match 9.7%; Score 126; DB 10; Length 716;
Matches 284; Conservative 0; Mismatches 225; Indels 3; Gaps 2
563 aacacaaaggagatattactctccaaagaatgctgcgccgcgtccagaagaagcatattg 622
143 AACAAGGGAATTTACTTAAACAAGACACCCCTCCAGCAGTGCAGCAAAAACAACACTTT 202

```

QY 623 gatcaattacgaagatttaccacatttctaaggattcagaagtttttca 682  
 DB 203 GAACAATTTCACAGATTTTCATTTTAAAGATACAGCTTCGTCGAACCTTCCT 262  
 QY 683 cgtgacgaatctccttacccttcttgaagtagaagattcagaacgaacccc 742  
 DB 263 AGTGTGCTCCATGCTCTCAACTTATTGGCGAGATGAGAAAGAACATTAATGCA 322  
 QY 743 ctgagact-factttagacatgaataaagacttattgtttggagacttcggagaga 801  
 DB 323 TGGGGTTGTCATTTGGATGCGACATCATGACATGCGCGACGTAAGTTCGGACATC 362  
 QY 802 aaatttgatagtttcaatattcattcttcttacccttcaagagaagaatgagat 861  
 DB 383 AAATTTGATCTTTTACATACCTCTCTATGCTCCAGCTGATGAGATTAAGAAAGT 442  
 QY 862 agttgagagaaggttcttgcgaatttatactcgtgagacttttaagcccatatga 921  
 DB 443 GATTGAAGAAAGAGGCTTTTGTGATTTCAAGGTTAGAGCAATTAACGCGATGGGT 502  
 QY 922 tgcgtccttctctatgatgatgattaccacgaagatcccatgaacaattaaag--ca 979  
 DB 503 GAAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 562  
 QY 980 gagatgtgacatcatttaattgaatcagtttaagacacacacacacacacacacacac 1039  
 DB 563 GAAGGTGTACCAAGTTTATTAAGAGCTGTTCAGAACCAATTTTGAAGTGTGGA 622  
 QY 1040 gaagctattatgctgacttaccacagact 1071  
 DB 623 GAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 654

## RESULT 11

B1927794 711 bp mRNA linear EST 18-OCT-2001  
 LOCUS EST547663 tomato flower, 3 - 8 mm buds Lycopersicon esculentum CDNA  
 DEFINITION clone cT0B23P11 5' end, mRNA sequence.  
 ACCESSION B1927794  
 VERSION B1927794.1 GI:16238117  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
 1 (bases 1 to 711)  
 van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,  
 Utecherback, T., Van Aken, S., Romling, C.M., Nierman, W., Fraser, C.M.,  
 Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.  
 Generation of ESTs from tomato flower tissue, 3-8 mm buds (2001)  
 Unpublished (2001)  
 CONTACT: CUGI  
 CLEMSON UNIVERSITY GENOMICS INSTITUTE  
 CLEMSON UNIVERSITY  
 100 JORDAN HALL, CLEMSON, SC 29634, USA  
 EMAIL: <http://www.genome.clemson.edu/orders/index.html>  
 This clone is available through the Clemson University Genomics  
 Institute  
 Seq primer: T3.

## FEATURES

SOURCE Location/Qualifiers  
 1..711  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="CT0B23P11"  
 /clone\_lib="tomato flower, 3 - 8 mm buds"  
 /tissue\_type="flower"  
 /dev\_stage="3-8mm buds"  
 /note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; supplier: Cornell University; sequencing: The

Institute for Genomic Research. Flower buds and flowers  
 were taken from greenhouse plants (4-8 wks old, TA496).  
 They were immediately frozen in liquid nitrogen and then  
 size-separated while remaining frozen.  
 BASE COUNT 251 a 97 c 135 g 228 t  
 ORIGIN

Query Match 9.6%; Score 125; DB 10; Length 711;  
 Best Local Similarity 53.5%; Pred No. 9.4e-14;  
 Matches 375; Conservative 0; Mismatches 290; Indels 36; Gaps 4;

QY 27 tatgaatgagatcccaagaagttccatgataatgaagtgagaagcgatacaagttacg 86  
 DB 29 TGAATATGAAGGTGTTGTAAGTTTCACATGATGAGAGAAAGGACATTAAGCTATG 88  
 QY 87 ccaagaatgacatcc--tacaatctgcttctgcgaagtgaaacttcccttgaaacat 143  
 DB 89 CAATATATTCCTTGCTGTCAGAAAAGGTATTCATATGACAAACCAATTAAGATCAAG 148  
 QY 144 gatacagaagattgttcgaggaacttgcacacatcaacaagtgataaagttcgag 203  
 DB 149 CCATATAGATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 199  
 QY 204 atttgagatgcgcttcgagacacaacacacacacacacacacacacacacacacacacac 263  
 DB 200 ATTGCGTGTCTCTTCTGAGACGACACACTTTTGTAGGTGATCAGAACTGTGTAAGGTCA 259  
 QY 264 ttgacaagtttgcgaagagaagaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 323  
 DB 260 TTGAAAAGAACG-----AAAAAACAGATCTCAATATCAACAGAGTTTATTTTACAT 313  
 QY 324 tgaatgattcttcccaaatgatttcaatgatttcaatgatttcaatgatttcaatgatttcaat 383  
 DB 314 TCATGATGATCTCCCTGGAATGATTTTACGCGATTTTTCATGCTGATGAGGGAATTTGAAAC 373  
 QY 384 gaaacatcgagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 443  
 DB 374 AAATTTGAAAAAACAATTTGAGAAAGACTTGTCATGTTTATTAAGTGTGCTGCTG 433  
 QY 444 gctcttctcagcagacacttcccgagagatcatgacttttgcactctgttaca 503  
 DB 434 GTTCATTTTATTTCTAGACATTTTTCATCAAAAAGTTTGATTTGTCACATCATTTATA 493  
 QY 504 gtgttcattggttactcgaagttcccaagcggttggatgaattggagattgtgacaa 563  
 DB 494 GTCTATGCTGCTATCTCAAGTTCCTAATTTA-----ATTGAAAAGA 535  
 QY 564 acaagaaggagatttactcttcccaagaagatgtgtcgcgcgcgcgcgcgcgcgcgcgcgcgc 623  
 DB 536 ACAAGGCGAATATTACATGCAAGTACCAAGTCCACCAAGTGTATTAAGCATATTACA 595  
 QY 624 atcaattacgaagaatttaccacatttctaaggattcagaagattgttttccac 683  
 DB 596 ACCAATATGAAAAAAGATTTTCAATTTTGTGAATATTCGTCGGAAGATGATGAAG 655  
 QY 684 gtggcgaatgctccttaccctgcatcttgaagtagatgaa 724  
 DB 656 GTGGAAAAATGATGATTAACATTTTGAAGAAAGAGAGTGA 696

## RESULT 12

BE202392 474 bp mRNA linear EST 07-SEP-2000  
 LOCUS EST392841 KY1 Medicago truncatula cDNA clone pxv1-265, mRNA  
 DEFINITION sequence.  
 ACCESSION BE202392  
 VERSION BE202392.1 GI:8745693  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;







```

Db 117 CCACACACACCTCCCAAGACCTTCGATGAGATCGGCTGTTCTTGACACAAACA 176
QY 221 cacttaacagtcgagacatgtgcaagatgacaaagtctgcaagaagaaga 290
Db 177 CTTTGCTGTGGTGCAGAAATCATCATGCTGGGAGAAAGCTTGCCACAAATGAAAT 236
QY 291 atgatatgaagcgtccaccatcagatcttctcgaatgacatcttcccaaatgattca 350
Db 237 ATGCATC-----TCCCAATACAAAGATCTTTTAAACATCTTTCAGGAATGACTTCA 290
QY 351 attcggtttcagaatgtgctgcacaaagcttctacccgaacacgaaagaatgagcga 410
Db 291 ACAACATTTTAAAGTACCTGATGATGATTAACATTAACATCTGATGATTAACAAATG 350
QY 411 agatagagatcgtgcttaataaagcgaatgctgtccttcttcaagcagactcttcccg 470
Db 351 AAATGACCTTGTCTACTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 410
QY 471 agagatcagatcttcttgaacatctgttcaagtgatcattgttctcaggttccca 530
Db 411 ATGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 470
QY 531 ggcgttctgtatgattgagatgagatgagatgagatgagatgagatgagatgagatg 590
Db 471 AAGGT-----ATAGATTAACATTAAGGATTAACATTAACATTAACATTAACATTA 512
QY 591 gatgcgtccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 650
Db 513 CAATGCTCCCTCAATGCTGCAAGGCTTACTGAGCATTTTCAAGAGACTGTCGATTT 572
QY 651 ttccaagatctcagaaagatgttcttcaagtcgcaagtcgcaagtcgcaagtcgcaag 710
Db 573 TTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632
QY 711 gtaagatgagatgattgagcgaacgcg 736
Db 633 GAAAGAAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658

RESULT 14
LOCUS BI205540 482 bp mRNA linear EST 11-JUL-2001
DEFINITION EST523380 CTOS Lycopersicon esculentum cDNA clone CTOSB4 5' end,
mRNA sequence.
ACCESSION BI205540
VERSION BI205540.1 GI:14683264
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 482)
REFERENCE 1 (bases 1 to 482)
AUTHORS van der Hoeven, R., Sun, H., Bezzierides, J., Cho, J., Utterback, R.,
Ronnig, C. and Tanksley, S.
TITLE Generation of ESTs from Tomato Suspension Cultures
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1. 482
/organism="Lycopersicon esculentum"
/cultivar="TA496, E6203"
/db_xref="taxon:4081"
/clone="CTOSB4"
/clone_id="CTOS"
/tissue_type="suspension cultures"
/lab_host="SOLR"
FEATURES
Source

```

```

/notes="vector: pbluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and 1mg/ml 2,4d (pH5.8).
Fresh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
shaking."
BASE COUNT 153 a 81 c 113 g 135 t
ORIGIN
Query Match 8.5%; Score 109.8; DB 10; Length 482;
Best Local Similarity 57.6%; Freq. No. 7.3e-11;
Matches 223; Conservative 0; Mismatches 152; Indels 12; Gaps 1;
QY 551 gggattgtgcaacaagaaggatattactcttccaagaagatgctgcgcgcgcgcg 610
Db 62 GGAATGTGAATTAACAAAGGAGCTATTATGATCAAGACCAAGCCATCAAGCGTCTC 121
QY 611 aagcatattgagatcattacgaagaatttaccacattcttaagatcattcgaa 670
Db 122 AAAGCATATTCCAGCAATTAAGAGATTTGCGGACTTTTCTCAAGTATCGTCAAGAA 181
QY 671 gattgtttcagctgacgaatgctccttaccatgattgtlaagatagatcagac 730
Db 182 GAATGTGTGAAGGTGAGCATGATGATTAAGCATGCTGTGAAGAAATGAGCATAC 241
QY 731 gaaccgaa-----tcccttagacttacttgaatgacatgacgaataaagattgatt 778
Db 242 TTAAGCAATGTGTGCGCTTATGTTGAGACCTTTGGCCATCGCGCTCAAGACTTGTT 301
QY 779 gttgagagactctggagaaagaatgagatgattgacatttcaattcttaccat 838
Db 302 ACAGAGGATGATGATGAAGAAAGAAATGATGCTTCAAGCTTCCAGCTACGTCGA 361
QY 839 taagagaagaagaatgacatgattgagagagagagagagagagagagagagagag 898
Db 362 TCTCCAGCAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 921
QY 899 gaggactttaaggccattatgact 925
Db 422 AGAATTTGAACACCAAGATGATCT 448

RESULT 15
LOCUS BI210946 678 bp mRNA linear EST 11-JUL-2001
DEFINITION EST528986 CTOS Lycopersicon esculentum cDNA clone CTOS24D12 5' end,
mRNA sequence.
ACCESSION BI210946
VERSION BI210946.1 GI:14688670
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 678)
REFERENCE 1 (bases 1 to 678)
AUTHORS van der Hoeven, R., Sun, H., Bezzierides, J., Cho, J., Utterback, R.,
Ronnig, C. and Tanksley, S.
TITLE Generation of ESTs from Tomato Suspension Cultures
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1. 678
/organism="Lycopersicon esculentum"
/cultivar="TA496, E6203"
FEATURES
Source

```

```
/db.xref="taxon:4081"  
/clone="CTOS24D12"  
/issue.lib="CTOS"  
/issue.type="suspension cultures"  
/lab.host="SOIR"  
/note="Vector: p Bluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; Suspension cultures of L. esculentum E6203 were grown  
in Murashige and Skoog based medium, supplemented with 15%  
coconut milk (filter sterilized and added after  
autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).  
Fresh medium was added every 7 days, and cultures were  
grown at 25 C, with 12hrs of light and continuous  
shaking."
```

BASE COUNT 217 a 102 c 149 g 210 t  
ORIGIN

Query Match 8.3%; Score 108.2; DB 10; Length 678;  
Best Local Similarity 57.4%; Pred. No. 1.3e-10;  
Matches 222; Conservative 0; Mismatches 153; Indels 12; Gaps 1;

```
OY 551 ggagttgtgcaacaagaaggagttatctcttcacaaagagatgtccgcgcgcag 610  
DB 62 GGATTTGAGAAATTAACAAGGAGCTATTATGCAATCAAGTACAGCCCATCAGCCTC 121  
OY 611 aagcatatttgatcaatttcgaagaatttcacacatttcgaagattcgcgaa 670  
DB 122 AAAGCATTTTCAAGCAATATTAAGAAAGATTTCGCGACTTTCTCAAGTATCGTTCA 181  
OY 671 gagttgtttcagctgagcgaatgtctcttactctgcaattgttaagtagatgcag 730  
DB 182 GAATTGTGAAAGGTGAGCTATGATTAACCATGCGCTGTAAGAAATAGCATCAG 241  
OY 731 gaaccgaa-----tccctagacttacttgacatgycataaagcattgatt 778  
DB 242 TTAAAGCAATGTGTGCTTTATGTTGAGACCTTTGGCCATCGCGCTCAAGAGATTG 301  
OY 779 gttagagacttcctggaagaagaatttgatagttcaataataccattccttaacct 838  
DB 302 ACAGAGGAGATCGATAGAGAGAGAAATGATTCGTTCAACGTTCCAAAGTACTCTCA 361  
OY 839 tcagcaagaagaatgaagtcagatagttgaagaagaagttccttcggaatttatactg 898  
DB 362 TCTCCACAGCAATATACGATATGATTTGAAGAAGAGGATCTTCACTATGACCTTTG 421  
OY 899 gagactttaaggccattatgact 925  
DB 422 AGAATTTTAAACACACAGATGATTC 448
```

Search completed: July 27, 2002, 03:57:08  
Job time: 2109 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2002, 04:39:44 ; Search time 50.23 Seconds  
(without alignments)  
835.873 Million cell updates/sec

Title: US-09-971-020-1

Perfect score: 1972

Sequence: 1 MEQETLHNEEGEDTSYK.....KCCYNLTLSAKRPSDV 378

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq.032802.\*  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649.5	32.9	364	22	AA667769
2	639	32.4	389	21	AA622189
3	638	32.4	405	21	AA622188
4	628	31.8	386	21	AA622180
5	614	31.1	356	22	AA645739
6	611.5	31.0	379	21	AA612686
7	611.5	30.9	349	21	AA612687
8	609.5	30.9	349	21	AA612687
9	609.5	29.7	327	21	AA612688
10	586	29.7	327	21	AA612688
11	586	29.7	327	21	AA637441

12	432	21.9	374	21	AA606670	Arabidopsis thalia
13	432	21.9	374	21	AA606653	Arabidopsis thalia
14	432	21.9	386	21	AA606659	Arabidopsis thalia
15	432	21.9	386	21	AA606652	Arabidopsis thalia
16	432	21.9	387	21	AA606651	Arabidopsis thalia
17	432	21.9	389	21	AA606668	Arabidopsis thalia
18	395.5	20.1	343	21	AA606664	Arabidopsis thalia
19	395.5	20.1	348	21	AA606663	Arabidopsis thalia
20	393	19.9	345	21	AA613021	Arabidopsis thalia
21	393	19.9	345	21	AA613020	Arabidopsis thalia
22	367.5	18.6	318	21	AA613022	Arabidopsis thalia
23	363.5	15.4	255	21	AA606665	Arabidopsis thalia
24	363.5	15.4	255	21	AA606665	Arabidopsis thalia
25	253.5	12.9	187	21	AA612997	Arabidopsis thalia
26	133	6.7	154	21	AA614384	Arabidopsis thalia
27	129	6.5	112	21	AA614383	Arabidopsis thalia
28	129	6.5	117	21	AA614382	Human protein sequ
29	106.5	5.4	585	22	AA695130	Human RNA helicase
30	106.5	5.4	778	22	AA699892	Human RNA helicase
31	106.5	5.4	851	22	AA699891	Human RNA helicase
32	103.5	5.2	946	21	AA618208	Human protein secret
33	101	5.1	997	22	AA633088	Human protein secret
34	100.5	5.1	556	22	AA694696	Human protein sequ
35	100.5	5.1	2144	22	AA685029	Human protein encoded by
36	98	5.0	2185	12	AA612141	Enteroviral polype
37	97	4.9	960	22	AA692632	Mutant human prost
38	96.5	4.9	960	22	AA69372	Human polyprotein
39	96	4.8	865	22	AA65448	Human prostatic can
40	94.5	4.8	865	22	AA65448	Helicobacter pylori
41	94	4.8	648	20	AA661198	Human herpesvirus
42	94	4.8	648	20	AA661199	Human herpesvirus
43	94	4.8	693	21	AA612647	Mutant human PSM a
44	94	4.8	693	21	AA612647	Human prostate spe
45	94	4.8	707	19	AA647155	Extracellular doma

#### ALIGNMENTS

RESULT 1	AA667769	standard; Protein; 364 AA.
ID	AA667769	
AC	AA667769	
DT	11-JUN-2001	(first entry)
DE	Snadpragon benzoleic acid carboxyl methyltransferase (BAMT) protein.	
KW	Snadpragon; benzoleic acid carboxyl methyltransferase; BAMT; floral scent;	
KW	S-adenosyl-L-methionine:benzoleic acid carboxyl methyltransferase;	
KW	methyl benzoleate; transgenic plant; ss	
OS	Antirrhinum majus.	
XX	WO200118183-A1.	
XX	15-MAR-2001.	
XX	01-SEP-2000; 2000MO-US24362.	
XX	03-SEP-1999; 99US-0152393.	
XX	(PURD) PURDUE RES FOUND.	
XX	Doudareva N, Murfitt LM, Mann CJ;	
XX	WPI: 2001-244568/25.	
XX	N-PSDB: AA680136.	
XX	Novel purified benzoleic acid carboxyl methyltransferase protein useful	
PT	for production of floral scent compounds and biosynthesis	
XX		

PS Claim 3; Page 85-88; 94pp; English.  
 CC The present sequence represents a Snaptdragon benzoyl acid carboxyl  
 CC methyltransferase (BAMT) protein. The protein is a  
 CC S-adenosyl-L-methionine:benzoic acid carboxyl methyltransferase, and  
 CC the enzyme is used in the formation of floral scent compounds such as  
 CC methyl benzoate. The enzyme catalyses the transfer of a methyl group  
 CC donor, such as S-adenosyl methionine (SAM) to benzoic acid to form  
 CC methyl benzoate. BAMT proteins are useful for the production of floral  
 CC scent compounds and biosynthesis.. BAMT polynucleotides are useful for  
 CC producing transgenic plants.  
 XX Sequence 364 AA:  
 SQ  
 Query Match 32.9%; Score 649.5; DB:22; Length 364;  
 Best Local Similarity 37.5%; Pred. No. 8.8e-57;  
 Matches 143; Conservative 85; Mismatches 122; Indels 31; Gaps 10;  
 QY 3 LOEVLMN-EGEGDTSYAKNAS-VNLAIAKVRPLEDQICIRRLNANLPINIKCIYVADLG 60  
 Db 4 mklilcmnlagdgsetsyahnsqilqkymmakshlvdelkklidldghv-gfrpcfkmmndmg 62  
 QY 61 CASGPFTLLTYVDIYOSIDKYGOEKNEDLEPTIOIFINLEFQWDFSVAYKLPLSEYRL 120  
 Db 63 ccsagpallvmsgintntedl-yteknlnelpefevflndipddfnfkl-----l 114  
 QY 121 EKXNGKRICSCISAMPSEFGYRLPEESMHPHSCYVNMHGOVPSGLYIELGIGANKG 180  
 Db 115 shen----gncfvyglpsfygryllpkklshltagssyhlhlsqvgpgle-----dnmrq 165  
 QY 181 STYSKSGCPRPQKAYUDQFTKDETFTEFLRHSKELFSGRMLTLCICQKVDPEDEPRPD- 239  
 Db 166 nlymatespreyykaykaygertstflklrgeelvpgrmvtlfngr--svedpskxd 223  
 QY 240 -----LLDAVINDLIVEGLLEEKLDSPNIPPEFTPSAEVVCYIEEGSGCEILYETFK 294  
 Db 224 laifllaktladvmaeglvymddlysfnlrplyspoctveaallesgstldrlievfv 283  
 QY 295 HYDAASIDDD---YPAVSHQIKAEYVASLRSYVEPTLASHGEMIMDPLHRLAKHA 351  
 Db 284 cwtasaytdddgdqgqsfyfgkysgkfivadcvtaltemplashgstlmallfykyakl 343  
 QY 352 AKYLAHMGKGCYNNLLIISLAKK 372  
 Db 344 vchlsvenssyistlsvlsitr 364  
 RESULT 2  
 AAG22189 standard; Protein; 389 AA.  
 ID AAG22189 standard; Protein; 389 AA.  
 AC AAG22189;  
 XX 17-OCT-2000 (first entry)  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 25023.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 25023.  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KM termination sequence.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PF 25-FEB-2000; 2000EP-0301439.  
 XX 25-FEB-1999; 9905-0121825.  
 XX 05-MAR-1999; 9905-0123380.  
 PR 09-MAR-1999; 9905-01233548.  
 PR 23-MAR-1999; 9905-0125788.  
 PR 25-MAR-1999; 9905-0126564.  
 PR 26-MAR-1999; 9905-0126785.  
 PR 01-APR-1999; 9905-0127462.  
 PR 06-APR-1999; 9905-0128234.  
 PR 06-APR-1999; 9905-0128714.  
 PR 15-APR-1999; 9905-0129845.  
 PR 19-APR-1999; 9905-0130077.  
 PR 21-APR-1999; 9905-0130449.  
 PR 23-APR-1999; 9905-0130510.  
 PR 23-APR-1999; 9905-0130691.  
 PR 28-APR-1999; 9905-0131449.  
 PR 30-APR-1999; 9905-0132048.  
 PR 04-MAY-1999; 9905-0132407.  
 PR 05-MAY-1999; 9905-0132485.  
 PR 06-MAY-1999; 9905-0132885.  
 PR 06-MAY-1999; 9905-0132487.  
 PR 07-MAY-1999; 9905-0132663.  
 PR 11-MAY-1999; 9905-0134256.  
 PR 11-MAY-1999; 9905-0134218.  
 PR 14-MAY-1999; 9905-0134419.  
 PR 14-MAY-1999; 9905-0134421.  
 PR 18-MAY-1999; 9905-0134370.  
 PR 18-MAY-1999; 9905-0134768.  
 PR 19-MAY-1999; 9905-0134941.  
 PR 20-MAY-1999; 9905-0135124.  
 PR 21-MAY-1999; 9905-0135553.  
 PR 24-MAY-1999; 9905-0135529.  
 PR 27-MAY-1999; 9905-0136021.  
 PR 27-MAY-1999; 9905-0136392.  
 PR 28-MAY-1999; 9905-0136782.  
 PR 01-JUN-1999; 9905-0137222.  
 PR 03-JUN-1999; 9905-0137528.  
 PR 04-JUN-1999; 9905-0137502.  
 PR 07-JUN-1999; 9905-0137724.  
 PR 08-JUN-1999; 9905-0138094.  
 PR 10-JUN-1999; 9905-0138840.  
 PR 10-JUN-1999; 9905-0138847.  
 PR 11-JUN-1999; 9905-0139452.  
 PR 11-JUN-1999; 9905-0139453.  
 PR 11-JUN-1999; 9905-0139492.  
 PR 16-JUN-1999; 9905-0139455.  
 PR 18-JUN-1999; 9905-0139456.  
 PR 18-JUN-1999; 9905-0139457.  
 PR 18-JUN-1999; 9905-0139458.  
 PR 18-JUN-1999; 9905-0139459.  
 PR 18-JUN-1999; 9905-0139460.  
 PR 18-JUN-1999; 9905-0139461.  
 PR 18-JUN-1999; 9905-0139462.  
 PR 18-JUN-1999; 9905-0139463.  
 PR 18-JUN-1999; 9905-0139750.  
 PR 18-JUN-1999; 9905-0139763.  
 PR 21-JUN-1999; 9905-0139817.  
 PR 22-JUN-1999; 9905-0139869.  
 PR 23-JUN-1999; 9905-0140353.  
 PR 23-JUN-1999; 9905-0140654.  
 PR 24-JUN-1999; 9905-0140655.  
 PR 28-JUN-1999; 9905-0140823.  
 PR 30-JUN-1999; 9905-0140981.  
 PR 01-JUL-1999; 9905-0141267.  
 PR 01-JUL-1999; 9905-0141542.  
 PR 01-JUL-1999; 9905-0142154.  
 PR 02-JUL-1999; 9905-0142505.  
 PR 06-JUL-1999; 9905-01442390.  
 PR 08-JUL-1999; 9905-0142803.  
 PR 09-JUL-1999; 9905-01442920.  
 PR 12-JUL-1999; 9905-0142977.  
 PR 13-JUL-1999; 9905-0143542.  
 PR 14-JUL-1999; 9905-0143624.  
 PR 15-JUL-1999; 9905-0144005.



DE Arabidopsis thaliana protein fragment SEQ ID NO: 25022.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX Arabidopsis thaliana.  
OS  
PN EP1033405-A2.  
PD  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 04-MAY-1999; 99US-0132048.  
PR 05-MAY-1999; 99US-0132407.  
PR 06-MAY-1999; 99US-0132484.  
PR 07-MAY-1999; 99US-0132485.  
PR 11-MAY-1999; 99US-0132487.  
PR 14-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134270.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138640.  
PR 10-JUN-1999; 99US-0138647.  
PR 14-JUN-1999; 99US-0139111.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147392.  
PR 06-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 06-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148684.  
PR 13-AUG-1999; 99US-0148685.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149930.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 26-AUG-1999; 99US-0151063.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.

```

PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151330.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157855.
PR 06-OCT-1999; 99US-0158029.
PR 07-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159339.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

```

Query Match 32.4%; Score 639; DB 21; Length 405;  
 Best Local Similarity 37.8%; Pred. No. 1.2e-55;  
 Matches 151; Conservative 79; Mismatches 129; Indels 40; Gaps 12;

```

OY 1 MELOEVLHNEEGGPTSYAKNASTNLALAKV-KPFLGOCIRELRLANLPNTKCIKRVADL 59
DB 17 MEMWVJLHNMKGSTYKSTGNSLISLGRVMDLKKLMMNS--SELSISGLADL 74
OY 60 GCAAGPRTLLTYRDVDSIDKVGQEKNELEKRP--IOFLINDLQONQNFVFLLSFY 117
DB 75 GCSGSPNLSLSNLDVCHLCP-----dlrpyelrvisIndlpndfnfycaslpely 130
OY 118 RKLKENGKRTG-----SCLISAMPQSPFYGRLPPEBSMHFLHSCYSVHMTSOVP-- 166
DB 131 ---drvnmhkegfyfgrggscectvsavpsfygrllfprtrshfthssssslhwlsqypcr 187
OY 167 -----SGLVIEIGICAMKNGSIYSKSCGRPPVOKAYLDOFTFDFTFLRIHNSKELFSGR 220
DB 188 eaekedtltaadi---emngkiyisktkapsahkayaIqfcdflvflrseelvpgr 244
OY 221 MLATGICK--VDFDEPN--PDLIDMAINDLYEGLEBEKEDSPNIPFTPSAEVKKC 276
DB 245 mvlsffgrslpdtteesxyqwellagelmsakegflseekldafnpyvaaseelkm 304

```

```

OY 277 IVEEGSCCELLYEFKKAHYDAFSDDDY--PYRSHQIRKA--EYVASLIRSYEPILA 332
DB 305 vlekegfslrdlelspldwegssiseesydlaIrkpaleasgrtrvatravemple 364
OY 333 SHFEALMPDLFHLAKHAKAHLHMKCKCYNNLISLAK 371
DB 365 plfgenwmdelferyakIqgefyfyspsryalvllslvr 403

RESULT 4
AAG22190
ID AAG22190 standard; Protein: 386 AA.
XX
AC AAG22190;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 25024.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PE 25-FEB-1999; 99US-0121825.
XX
PR 05-MAR-1999; 99US-0123180.
XX
PR 09-MAR-1999; 99US-0123548.
XX
PR 23-MAR-1999; 99US-0125788.
XX
PR 25-MAR-1999; 99US-0126264.
XX
PR 29-MAR-1999; 99US-0126785.
XX
PR 01-APR-1999; 99US-0127462.
XX
PR 06-APR-1999; 99US-0128234.
XX
PR 08-APR-1999; 99US-0128714.
XX
PR 16-APR-1999; 99US-0129845.
XX
PR 19-APR-1999; 99US-0130077.
XX
PR 21-APR-1999; 99US-0130449.
XX
PR 23-APR-1999; 99US-0130510.
XX
PR 23-APR-1999; 99US-0130891.
XX
PR 28-APR-1999; 99US-0131449.
XX
PR 30-APR-1999; 99US-0132048.
XX
PR 30-APR-1999; 99US-0132407.
XX
PR 04-MAY-1999; 99US-0132484.
XX
PR 05-MAY-1999; 99US-0132485.
XX
PR 06-MAY-1999; 99US-0132486.
XX
PR 06-MAY-1999; 99US-0132487.
XX
PR 07-MAY-1999; 99US-0132863.
XX
PR 11-MAY-1999; 99US-0134256.
XX
PR 14-MAY-1999; 99US-0134218.
XX
PR 14-MAY-1999; 99US-0134219.
XX
PR 14-MAY-1999; 99US-0134221.
XX
PR 14-MAY-1999; 99US-0134370.
XX
PR 18-MAY-1999; 99US-0134768.
XX
PR 19-MAY-1999; 99US-0134841.
XX
PR 20-MAY-1999; 99US-0135124.
XX
PR 21-MAY-1999; 99US-0135253.
XX
PR 24-MAY-1999; 99US-0135629.
XX
PR 25-MAY-1999; 99US-0136021.
XX
PR 27-MAY-1999; 99US-0136392.
XX
PR 28-MAY-1999; 99US-0136782.
XX
PR 01-JUN-1999; 99US-0137222.
XX
PR 03-JUN-1999; 99US-0137528.
XX
PR 04-JUN-1999; 99US-0137502.
XX
PR 07-JUN-1999; 99US-0137724.
XX
PR 08-JUN-1999; 99US-0138094.
XX
PR 10-JUN-1999; 99US-0138540.
XX
PR 10-JUN-1999; 99US-0138847.

```

PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 21-JUN-1999; 99US-0139763.  
PR 22-JUN-1999; 99US-0139817.  
PR 23-JUN-1999; 99US-0139819.  
PR 23-JUN-1999; 99US-0140353.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142920.  
PR 13-JUL-1999; 99US-0142927.  
PR 14-JUL-1999; 99US-0143542.  
PR 15-JUL-1999; 99US-0143542.  
PR 16-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144005.  
PR 19-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 21-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 22-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145226.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147204.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147203.  
PR 06-AUG-1999; 99US-0147203.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148564.  
PR 14-AUG-1999; 99US-0149358.  
PR 14-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149902.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151080.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154739.  
PR 20-SEP-1999; 99US-0155132.  
PR 22-SEP-1999; 99US-0155132.  
PR 23-SEP-1999; 99US-0155466.  
PR 24-SEP-1999; 99US-0155659.  
PR 26-SEP-1999; 99US-0156458.  
PR 28-SEP-1999; 99US-0156458.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159637.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160747.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161922.  
PR 28-OCT-1999; 99US-0161923.  
PR 29-OCT-1999; 99US-0162142.

Query Match 31.88; Score 628; DB 21; Length 386;  
Best Local Similarity 37.88; Pred. No. 1.4e-54;  
Matches 149; Conservative 78; Mismatches 127; Indels 40; Gaps 12;  
Db 6 VLMHNEGDTSYAKNASYNIALAKV-KPFLDQCIRELLRANLPNINKCIKIVADGACAG 64  
3 vlmhnggetayaknastagatllsigrvmdealkkiman--seissigldgcsag 60



**RESULT**

**ID** AAB5799 standard; protein: 356 AA.

**AA** AAB5799;

**D** 16-MAR-2001 (first entry)

**E** C. sinensis N-methyl transferase protein.

**F** Caffeine biosynthesis; N-methyl transferase; tea; N-met; plant.

**G** Camellia sinensis.

**H** EP1055727-A2.

**I** 29-NOV-2000.

**J** 26-MAY-2000; 2000EP-0304522.

**K** 26-MAY-1999; 99JP-0146358.

**L** (MITSU) CHEM INC.

**M** Mizuno M, Ashihara H, Mizuno K, Fujimura T;

**N** WPI; 2001-063619/08.

**O** This invention describes a novel DNA molecule (I) encoding N-methyl transferase (N-met) with the enzyme activities of 7-methyl xanthine N3 methyl transferase, theobromine N1 methyl transferase and paraxanthine N3 methyl transferase. The DNA or RNA encoding the N-met is useful for the enhancement of caffeine production in microorganisms or plants, and the DNA may also be used for producing N-met that can be used as an enzyme for industrial, food or medical use, e.g. for producing compounds related to caffeine metabolism by modifying caffeine biosynthesis and metabolism of caffeine productive plants, plant tissues or cells and for modifying caffeine biosynthesis and metabolism of caffeine productive plants, plant tissues or cells, therefore modifying the production rate.

**P** Claim 1; Page 19; 33pp; English.

XX	Sequence	356 AA:	31.1%: Score 614; DB 22; Length 356; Best Local Similarity 36.2%; Pred. No. 3.2e-53; Matches 140; Conservative 78; Mismatches 111; Indels 58; Gaps 11.
XX	Query Match		
XX	Best Local Similarity	36.2%;	Pred. No. 3.2e-53;
XX	Matches 140; Conservative	78; Mismatches 111;	Indels 58; Gaps 11.
SO	Sequence	356 AA:	
QY	MNGEEDTSYAKMSYNALAKY-KPELEOCIRELLEANLPINKIKYADIGASGPT	67	
DB	2 mnggeessyaynsftcgyasnaapalnavelfsrdth- lqalnadgcaapnt	59	
QY	68 LLIVRIYVSDIKQGEKNEMLRPT-IQIFINDLQONPNVSFVFLPFSFKLEKENG	125	
DB	60 fa-----vslrlmmeKkrcellncqlelqylnlqndlnlftgiss-----	105	
QY	126 RKIGS-----CLISAMGSPYGRPLFPESMEFLHSCYSVHMTLSQVPSGLVIEIGANK	179	
DB	106 evgnlgnceevpywgywgsfhrllprnslilvnsygvwltqgpkltstreglank	165	
QY	180 GSIVSSKGRPPVQKAYLDOFTKDTFTFLRIHSEKELFSRGMILTCICXVDFEENPL	238	
DB	166 gklylaktaprvvreylsqfhdetfmlnarsgevpvncvml--llgrqcspsdmq	223	
QY	239 -----DLMLAINDLIVEGLLEBEKIDSPNIFPFPPSAEEKCIIVEEGSCILYLETFK	293	
DB	224 scftwellamaelavsgliddckidtfnlpsylasleevkdldverdsftldhle--	280	
QY	294 AHYDAFSSIDDYPRSHEDQKAEVVASLIRSVPEPIIASHFGAIMPDLFRLAKNAK	353	
DB	281 -----gfdldsvemqndkwrgekftkvratleptllnsqfpeimdklyk-----	328	
QY	354 VLHMGKGCYNLIIS--LAKKPEKSDV	378	
DB	329 -----fthvsvdleakrpkltstl	347	
RESULT	6		
AC	AKG12686		
ID	AKG12686 standard; Protein; 379 AA.		
XX	AC		
XX	AKG12686;		
DT	17-OCT-2000 (first entry)		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 11897.		
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.		
OS	Arabidopsis thaliana.		
PN	EP1033405-A2.		
PD	06-SEP-2000.		
PF	25-FEB-2000; 2000EP-0301439.		
PR	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0123180.		
PR	09-MAR-1999; 99US-0123578.		
PR	23-MAR-1999; 99US-0125788.		
PR	23-MAR-1999; 99US-0126262.		
PR	23-MAR-1999; 99US-0126785.		
PR	01-APR-1999; 99US-0128432.		
PR	08-APR-1999; 99US-0128774.		
PR	16-APR-1999; 99US-0129685.		
PR	19-APR-1999; 99US-0130077.		
PR	21-APR-1999; 99US-0130449.		
PR	23-APR-1999; 99US-0130510.		

PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132483.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 18-MAY-1999; 99US-0134370.  
PR 19-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137528.  
PR 07-JUN-1999; 99US-0137502.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 14-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139452.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139839.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140635.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 08-JUL-1999; 99US-0142390.  
PR 09-JUL-1999; 99US-0142803.  
PR 12-JUL-1999; 99US-0142827.  
PR 12-JUL-1999; 99US-0143242.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 18-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144335.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145102.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 26-JUL-1999; 99US-0145224.  
PR 27-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 28-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0146389.  
PR 04-AUG-1999; 99US-0147028.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147419.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148565.  
PR 16-AUG-1999; 99US-0148684.  
PR 17-AUG-1999; 99US-0149368.  
PR 18-AUG-1999; 99US-0149175.  
PR 20-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155113.  
PR 23-SEP-1999; 99US-0155466.  
PR 23-SEP-1999; 99US-0155659.  
PR 26-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156599.  
PR 04-OCT-1999; 99US-0157111.  
PR 05-OCT-1999; 99US-0157765.  
PR 06-OCT-1999; 99US-0157865.  
PR 08-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158234.  
PR 12-OCT-1999; 99US-0158363.  
PR 13-OCT-1999; 99US-0158293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.

PR	14-OCT-1999	99US-0159584
PR	18-OCT-1999	99US-0159583
PR	21-OCT-1999	99US-0160741
PR	21-OCT-1999	99US-0160747
PR	21-OCT-1999	99US-0160751
PR	21-OCT-1999	99US-0160770
PR	21-OCT-1999	99US-0160768
PR	21-OCT-1999	99US-0160814
PR	21-OCT-1999	99US-0160815
PR	22-OCT-1999	99US-0160980
PR	22-OCT-1999	99US-0160981
PR	22-OCT-1999	99US-0160982
PR	22-OCT-1999	99US-0160984
PR	22-OCT-1999	99US-0161004
PR	23-OCT-1999	99US-0161405
PR	23-OCT-1999	99US-0161406
PR	23-OCT-1999	99US-0161359
PR	23-OCT-1999	99US-0161359
PR	23-OCT-1999	99US-0161361
PR	23-OCT-1999	99US-0161362
PR	23-OCT-1999	99US-0161363
PR	23-OCT-1999	99US-0161392
PR	23-OCT-1999	99US-0162142

Query Match	31.0%;	Score 611.5;	DB 21;	Length 379;
Best Local Similarity	38.8%;	Pred. No. 6,3e-53;		
Matches 147;	Conservative 71;	Mismatches 124;	Indels 37;	Gaps 12.

```

Oy      5 EYVHNHEEGOTSAVNNAS-VYTLAATKUYKFELOCIRELTPANIPINIKKIVAOAGAS 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      27 kalcmsggdgansysansarlgkkvlsnakevlyrtnleem--mnl-dfrcyikvaalgss 84
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      64 GWTNLTLYRDIYVGSIRKVOGE-EKNELERPPTIOIFINDFONDSVFKLSEFYRKEK 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      85 gqnsflaifeintlnlvlgqhnks---pelccndipendnttffkfyvifakeml 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      123 ENGRKIGCCLISAPGSPFCGRIFPESMHWLHSCYVNHLSQVSPGCVIELGANKGSI 182
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      142 tsk---sscfvugapsfysrfsrtnshlhhasyalhwlskveki-----eankgnl 192
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      183 YSASKCRPVOKALIOEPRKDTPTFLRHNSKEFLFSGRYMLTLCIKVDEDEPNRPD-- 233
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      193 yltasspsqaykaylngqfkdtfmflrlrseelivangtmvltfgr-nltnbrlydcsh 251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      240 ---LIDMAMINDLYEGELEEEKLDSFNIPPTPSAEEGCVYEEGSECLTYLEFP-- 293
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      252 fctllsnslrtlvgeglvveeskladfmprfjdrnygelvklqkegfneleesngfdl 311
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      294 AHYDAFSEIDDDYVYNSHDLIAEYVASLYRSYRPEILASHNGEAMIPDLFHLKNAK 355
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      312 ghyue-----eddaagrne-----agltavsepmllantgeidlcldkyayntvq 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      354 VLMHGKGCINNLITSLAKK 372
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      361 hancrktlvsivslvslkk 379
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

XX	RESULT	7
XX	AAG37439	
ID	AAG37439	standard; protein; 379 AA.
XX		
AC	AAG37439;	
XX		
DT	18-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 46035.
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
XX	termination sequence.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EPI033405-A2.	
XX		

PD	06-SEP-2000.	
XX		
XX	25-FEB-2000.	2000EP-0301439.
XX		
PR	25-FEB-1999.	9905-0121825.
PR	05-MAR-1999.	9905-0123180.
PR	09-MAR-1999.	9905-0123548.
PR	23-MAR-1999.	9905-0125538.
PR	25-MAR-1999.	9905-0126564.
PR	28-MAR-1999.	9905-0126765.
PR	01-APR-1999.	9905-0127652.
PR	06-APR-1999.	9905-0128934.
PR	08-APR-1999.	9905-0128714.
PR	15-APR-1999.	9905-0129845.
PR	19-APR-1999.	9905-0130047.
PR	21-APR-1999.	9905-0130049.
PR	23-APR-1999.	9905-0130510.
PR	28-APR-1999.	9905-0131449.
PR	30-APR-1999.	9905-0132048.
PR	03-APR-1999.	9905-0132407.
PR	04-MAY-1999.	9905-0132484.
PR	05-MAY-1999.	9905-0132485.
PR	06-MAY-1999.	9905-0132486.
PR	07-MAY-1999.	9905-0132487.
PR	11-MAY-1999.	9905-0132487.
PR	14-MAY-1999.	9905-0134219.
PR	14-MAY-1999.	9905-0134218.
PR	14-MAY-1999.	9905-0134321.
PR	14-MAY-1999.	9905-0134370.
PR	18-MAY-1999.	9905-0134768.
PR	19-MAY-1999.	9905-0134941.
PR	20-MAY-1999.	9905-0135124.
PR	21-MAY-1999.	9905-0135353.
PR	25-MAY-1999.	9905-0135639.
PR	25-MAY-1999.	9905-0136021.
PR	27-MAY-1999.	9905-0136792.
PR	28-MAY-1999.	9905-0136782.
PR	01-JUN-1999.	9905-0137222.
PR	03-JUN-1999.	9905-0137528.
PR	04-JUN-1999.	9905-0137502.
PR	07-JUN-1999.	9905-0137724.
PR	08-JUN-1999.	9905-0138064.
PR	10-JUN-1999.	9905-0138540.
PR	14-JUN-1999.	9905-0138747.
PR	16-JUN-1999.	9905-0139119.
PR	16-JUN-1999.	9905-0139132.
PR	17-JUN-1999.	9905-0139433.
PR	18-JUN-1999.	9905-0139432.
PR	18-JUN-1999.	9905-0139434.
PR	18-JUN-1999.	9905-0139435.
PR	18-JUN-1999.	9905-0139436.
PR	18-JUN-1999.	9905-0139437.
PR	18-JUN-1999.	9905-0139438.
PR	18-JUN-1999.	9905-0139439.
PR	18-JUN-1999.	9905-0139440.
PR	18-JUN-1999.	9905-0139441.
PR	18-JUN-1999.	9905-0139442.
PR	18-JUN-1999.	9905-0139443.
PR	18-JUN-1999.	9905-0139444.
PR	18-JUN-1999.	9905-0139445.
PR	21-JUN-1999.	9905-0139817.
PR	21-JUN-1999.	9905-0139819.
PR	23-JUN-1999.	9905-0140353.
PR	23-JUN-1999.	9905-0140635.
PR	26-JUN-1999.	9905-0140823.
PR	29-JUN-1999.	9905-0140931.
PR	30-JUN-1999.	9905-0141287.
PR	01-JUL-1999.	9905-0141842.
PR	02-JUL-1999.	9905-0142154.
PR	02-JUL-1999.	9905-0142053.

PR 06-JUL-1999; 99US-0144390;  
PR 08-JUL-1999; 99US-01442803;  
PR 09-JUL-1999; 99US-01442920;  
PR 12-JUL-1999; 99US-01442977;  
PR 13-JUL-1999; 99US-01443442;  
PR 14-JUL-1999; 99US-01443624;  
PR 15-JUL-1999; 99US-01444005;  
PR 16-JUL-1999; 99US-01440885;  
PR 19-JUL-1999; 99US-0144325;  
PR 19-JUL-1999; 99US-0144331;  
PR 19-JUL-1999; 99US-0144332;  
PR 19-JUL-1999; 99US-0144333;  
PR 19-JUL-1999; 99US-0144334;  
PR 19-JUL-1999; 99US-0144335;  
PR 20-JUL-1999; 99US-0144332;  
PR 20-JUL-1999; 99US-0144632;  
PR 20-JUL-1999; 99US-0144884;  
PR 21-JUL-1999; 99US-0144814;  
PR 21-JUL-1999; 99US-0145088;  
PR 22-JUL-1999; 99US-0145088;  
PR 22-JUL-1999; 99US-0145087;  
PR 22-JUL-1999; 99US-0145089;  
PR 22-JUL-1999; 99US-0145192;  
PR 23-JUL-1999; 99US-0145145;  
PR 23-JUL-1999; 99US-0145218;  
PR 23-JUL-1999; 99US-0145224;  
PR 26-JUL-1999; 99US-0145276;  
PR 27-JUL-1999; 99US-0145913;  
PR 27-JUL-1999; 99US-0145918;  
PR 28-JUL-1999; 99US-0145919;  
PR 02-AUG-1999; 99US-0145951;  
PR 02-AUG-1999; 99US-0146386;  
PR 02-AUG-1999; 99US-0146388;  
PR 03-AUG-1999; 99US-0147038;  
PR 04-AUG-1999; 99US-0147204;  
PR 04-AUG-1999; 99US-0147302;  
PR 05-AUG-1999; 99US-0147192;  
PR 05-AUG-1999; 99US-0147260;  
PR 06-AUG-1999; 99US-0147303;  
PR 06-AUG-1999; 99US-0147416;  
PR 09-AUG-1999; 99US-0147493;  
PR 09-AUG-1999; 99US-0147935;  
PR 10-AUG-1999; 99US-0148171;  
PR 11-AUG-1999; 99US-0148319;  
PR 12-AUG-1999; 99US-0148341;  
PR 13-AUG-1999; 99US-0148565;  
PR 13-AUG-1999; 99US-0148684;  
PR 16-AUG-1999; 99US-0149368;  
PR 17-AUG-1999; 99US-0149175;  
PR 18-AUG-1999; 99US-0149426;  
PR 20-AUG-1999; 99US-0149722;  
PR 20-AUG-1999; 99US-0149723;  
PR 20-AUG-1999; 99US-0149902;  
PR 23-AUG-1999; 99US-0149902;  
PR 23-AUG-1999; 99US-0149930;  
PR 25-AUG-1999; 99US-0150566;  
PR 26-AUG-1999; 99US-0150884;  
PR 27-AUG-1999; 99US-0151065;  
PR 27-AUG-1999; 99US-0151066;  
PR 27-AUG-1999; 99US-0151080;  
PR 30-AUG-1999; 99US-0151303;  
PR 31-AUG-1999; 99US-0151438;  
PR 01-SEP-1999; 99US-0151930;  
PR 07-SEP-1999; 99US-0152363;  
PR 10-SEP-1999; 99US-0153070;  
PR 13-SEP-1999; 99US-0153758;  
PR 15-SEP-1999; 99US-0154018;  
PR 16-SEP-1999; 99US-0154039;  
PR 20-SEP-1999; 99US-0154779;  
PR 22-SEP-1999; 99US-0155139;

PR 23-SEP-1999; 99US-0155486;  
PR 24-SEP-1999; 99US-0155659;  
PR 26-SEP-1999; 99US-0156458;  
PR 29-SEP-1999; 99US-0156596;  
PR 04-OCT-1999; 99US-0157117;  
PR 05-OCT-1999; 99US-0157753;  
PR 06-OCT-1999; 99US-0157865;  
PR 07-OCT-1999; 99US-0158029;  
PR 08-OCT-1999; 99US-0158322;  
PR 12-OCT-1999; 99US-0158369;  
PR 13-OCT-1999; 99US-0159293;  
PR 13-OCT-1999; 99US-0159294;  
PR 13-OCT-1999; 99US-0159295;  
PR 14-OCT-1999; 99US-0159329;  
PR 14-OCT-1999; 99US-0159330;  
PR 14-OCT-1999; 99US-0159331;  
PR 14-OCT-1999; 99US-0159637;  
PR 14-OCT-1999; 99US-0159638;  
PR 18-OCT-1999; 99US-0159584;  
PR 21-OCT-1999; 99US-0160741;  
PR 21-OCT-1999; 99US-0160767;  
PR 21-OCT-1999; 99US-0160768;  
PR 21-OCT-1999; 99US-0160770;  
PR 21-OCT-1999; 99US-0160814;  
PR 21-OCT-1999; 99US-0160815;  
PR 22-OCT-1999; 99US-0160980;  
PR 22-OCT-1999; 99US-0160981;  
PR 25-OCT-1999; 99US-0161404;  
PR 25-OCT-1999; 99US-0161405;  
PR 25-OCT-1999; 99US-0161406;  
PR 26-OCT-1999; 99US-0161359;  
PR 26-OCT-1999; 99US-0161360;  
PR 26-OCT-1999; 99US-0161361;  
PR 26-OCT-1999; 99US-0161362;  
PR 28-OCT-1999; 99US-0161992;  
PR 28-OCT-1999; 99US-0161993;  
PR 29-OCT-1999; 99US-0162142;

Query Match 31.0%; Score 611.5; DB 21; Length 379;  
Best Local Similarity 38.8%; Pred. No. 6,3e-53;  
Matches 147; Conservative 71; Mismatches 124; Indels 37; Gaps 12;

QY 5 EVLHNNREGDTSYAKNAS--YNLALAKVPFLEOCIRELRLRANLPNKNCKIVADIGCAS 63  
Db 27 kalcmsggdgnsysansrliqkklvismakpviyrnteeem-mnl-dfpylikvaelgcs 84  
QY 64 GNTLLTYRDIYOSIDKVGGE-EKNELEPRTIQIRINDLPNDPNSYERLISFYRKLEK 122  
Db 85 gmsltaifelinlinvliqhnks---pelocinoldpendntctkvpfinelmt 141  
QY 123 ENKRRIGCLISAMPSEFYGRLEPPEBSMHFLHSCYSVHWLSQVPSGLVTELGANKGST 182  
Db 142 ltk---ssctlygapselyerltsrnsnlhlnssyalhwlskvpekl-----enknhl 192  
QY 183 YSSKCCRPVOKAYLDQFTKDTFTFLIRHISKELEFSRGRMLTJCICKVDEBEPNLD-- 239  
Db 193 yltsspspsaykaylnqfkdftmfliriseelvangymvltfgyr-ntlndplyrdch 251  
QY 240 --LIDMAINDLIVEGLIEBEKLDSEFNIFFTPSAEVKCIVEBEGSCILYLEF--K 293  
Db 252 fctllnsrlrdlvfejlvesesklidatmpfyqpnvgelkevlyqegsfeneleahgd1 311  
QY 294 AYHDAFSDIDDPYVRSHEOIKAEVYASLRSVEPTIASHPGALPMDLFRHLKNAK 353  
Db 312 ghyve---eddfeagrne-----angltvsepmhlshfgeitdtlcfkyuyhvtq 360  
QY 354 VLMKKGCCYNMLLISLAK 372  
Db 361 hancnktvtvalvsllck 379

RESULT 8

AA012667  
ID AA012687 standard; Protein: 349 AA.  
AA012687;  
DT 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 11898.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11898.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
PN EPI033405-A2.  
XX EPI033405-A2.  
PD 06-SEP-2000.  
XX 06-SEP-2000.  
PF 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0122180.  
XX 09-MAR-1999; 99US-0123548.  
XX 23-MAR-1999; 99US-0125788.  
XX 25-MAR-1999; 99US-0126264.  
XX 29-MAR-1999; 99US-0126785.  
XX 01-APR-1999; 99US-0127462.  
XX 06-APR-1999; 99US-0128234.  
XX 08-APR-1999; 99US-0128714.  
XX 16-APR-1999; 99US-0129845.  
XX 19-APR-1999; 99US-0130077.  
XX 21-APR-1999; 99US-0130449.  
XX 23-APR-1999; 99US-0130510.  
XX 28-APR-1999; 99US-0130891.  
XX 30-APR-1999; 99US-0131448.  
XX 30-APR-1999; 99US-0132048.  
XX 04-MAY-1999; 99US-0132407.  
XX 04-MAY-1999; 99US-0132488.  
XX 05-MAY-1999; 99US-0132488.  
XX 06-MAY-1999; 99US-0132488.  
XX 07-MAY-1999; 99US-0132487.  
XX 11-MAY-1999; 99US-0132863.  
XX 14-MAY-1999; 99US-0134256.  
XX 14-MAY-1999; 99US-0134218.  
XX 14-MAY-1999; 99US-0134221.  
XX 14-MAY-1999; 99US-0134221.  
XX 14-MAY-1999; 99US-0134370.  
XX 18-MAY-1999; 99US-0134768.  
XX 19-MAY-1999; 99US-0134941.  
XX 20-MAY-1999; 99US-0135124.  
XX 21-MAY-1999; 99US-0135353.  
XX 24-MAY-1999; 99US-0135629.  
XX 25-MAY-1999; 99US-0136021.  
XX 27-MAY-1999; 99US-0136392.  
XX 28-MAY-1999; 99US-0136782.  
XX 01-JUN-1999; 99US-0137222.  
XX 03-JUN-1999; 99US-0137528.  
XX 04-JUN-1999; 99US-0137502.  
XX 07-JUN-1999; 99US-0137724.  
XX 08-JUN-1999; 99US-0138094.  
XX 10-JUN-1999; 99US-0138540.  
XX 10-JUN-1999; 99US-0138847.  
XX 14-JUN-1999; 99US-0139119.  
XX 16-JUN-1999; 99US-0139452.  
XX 16-JUN-1999; 99US-0139453.  
XX 17-JUN-1999; 99US-0139492.  
XX 18-JUN-1999; 99US-0139454.  
XX 18-JUN-1999; 99US-0139455.  
XX 18-JUN-1999; 99US-0139456.  
XX 18-JUN-1999; 99US-0139457.  
XX 18-JUN-1999; 99US-0139458.  
XX 18-JUN-1999; 99US-0139459.  
XX 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139464.  
PR 18-JUN-1999; 99US-0139465.  
PR 18-JUN-1999; 99US-0139466.  
PR 18-JUN-1999; 99US-0139467.  
PR 22-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142820.  
PR 12-JUL-1999; 99US-0142877.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143542.  
PR 15-JUL-1999; 99US-0144003.  
PR 16-JUL-1999; 99US-0144086.  
PR 16-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 21-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 22-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145192.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145513.  
PR 27-JUL-1999; 99US-0145518.  
PR 27-JUL-1999; 99US-0145519.  
PR 28-JUL-1999; 99US-0145551.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147203.  
PR 06-AUG-1999; 99US-0147416.  
PR 06-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 09-AUG-1999; 99US-0148171.  
PR 10-AUG-1999; 99US-0148319.  
PR 11-AUG-1999; 99US-0148341.  
PR 12-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.

PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149920.  
PR 23-AUG-1999; 99US-0150386.  
PR 23-AUG-1999; 99US-0150864.  
PR 27-AUG-1999; 99US-0151085.  
PR 27-AUG-1999; 99US-0151086.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154039.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 23-SEP-1999; 99US-0155139.  
PR 24-SEP-1999; 99US-0155569.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156396.  
PR 04-OCT-1999; 99US-0157117.  
PR 04-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 23-OCT-1999; 99US-0160880.  
PR 23-OCT-1999; 99US-0160981.  
PR 23-OCT-1999; 99US-0160989.  
PR 23-OCT-1999; 99US-0161404.  
PR 23-OCT-1999; 99US-0161405.  
PR 23-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 30.98; Score 609.5; DB 21; Length 349;  
Best Local Similarity 38.98; Pred. No. 8,9e-53;  
Matches 146; Conservative 70; Mismatches 122; Indels 37; Gaps 12.

OY 9 MNEGBDTSYAAKNAS-VYLAARVPELECEIRELLRAALPRINICIVADICGASGPT 67  
DB 1 ms99gansysnsrlqkkyismakpviynteeem-mml-dfpyikvaalgses99us 58  
OY 68 LTVRIIVGSIKVGGE-EKNELEPRTIOFLNDLFQDNFVSEKLEPSYRKLEKENG 126  
DB 59 flafetlntlnlvclqhnkns--peidccindipendntftrfypfinkelmtkn- 114  
OY 127 KISSCLISAMPSSFGRLFPESNMHLASCVSVHMLSOVPSGLVTELGIGANKSIYSK 186  
DB 115 -asctiyagpsstysrlftrnsnlhshsyalhmlskvpekl-----enknlylts 166  
OY 187 GCRPPYOKAVLDQFTKFTFLRIHSEKLEPSRGRLMLTICVKEDEPBNLD-----L 240

DB 167 sspesaykaylnqkdfcmftririseelvsngmvtlfigr-ntlomplydcchfvl 225  
OY 241 LDMAINDLIVEGLLEEKIDSNIFFTPSAEVYKCIVEEGSCELIYET--KAHYD 297  
DB 226 lsmrlalvteglvseskldatmnpdybnvqelkevldkgsfetelesngldghy 285  
OY 298 AAFSIDDPYRSEHQIKAEVVASLRSVEPIIASHFGCAIMPDLFHLAKNAKVLHM 357  
DB 286 e-----eddfaeagne-----anglravsepmiahfgeelldtlfdkyayhvtqhanc 334  
OY 358 GKGCYNNLITSLAKK 372  
DB 335 rnkktvalvslck 349  
RESULT 9  
AAC37440  
ID AAC37440 standard; Protein; 349 AA.  
XX AAC37440;  
AC AAC37440;  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46036.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
XX  
PN EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PE  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 23-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134270.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.

PR	01-JUN-1999	99US-0137222
PR	03-JUN-1999	99US-0137528
PR	04-JUN-1999	99US-0147260
PR	04-JUN-1999	99US-0147303
PR	07-JUN-1999	99US-0137752
PR	08-JUN-1999	99US-0138094
PR	10-JUN-1999	99US-0138847
PR	10-JUN-1999	99US-0139119
PR	14-JUN-1999	99US-0139452
PR	16-JUN-1999	99US-0139453
PR	17-JUN-1999	99US-0139492
PR	18-JUN-1999	99US-0139454
PR	18-JUN-1999	99US-0139455
PR	18-JUN-1999	99US-0139456
PR	18-JUN-1999	99US-0139457
PR	18-JUN-1999	99US-0139458
PR	18-JUN-1999	99US-0139459
PR	18-JUN-1999	99US-0139460
PR	18-JUN-1999	99US-0139461
PR	18-JUN-1999	99US-0139462
PR	18-JUN-1999	99US-0139750
PR	18-JUN-1999	99US-0139763
PR	21-JUN-1999	99US-0139897
PR	22-JUN-1999	99US-0140353
PR	23-JUN-1999	99US-0140354
PR	24-JUN-1999	99US-0140655
PR	28-JUN-1999	99US-0140823
PR	29-JUN-1999	99US-0140981
PR	30-JUN-1999	99US-0141287
PR	01-JUL-1999	99US-0144254
PR	02-JUL-1999	99US-0142350
PR	06-JUL-1999	99US-0142350
PR	08-JUL-1999	99US-0142803
PR	09-JUL-1999	99US-0142910
PR	12-JUL-1999	99US-0142927
PR	13-JUL-1999	99US-0143542
PR	14-JUL-1999	99US-0143624
PR	15-JUL-1999	99US-0144005
PR	16-JUL-1999	99US-0144085
PR	16-JUL-1999	99US-0144086
PR	19-JUL-1999	99US-0144331
PR	19-JUL-1999	99US-0144332
PR	19-JUL-1999	99US-0144333
PR	19-JUL-1999	99US-0144334
PR	19-JUL-1999	99US-0144335
PR	20-JUL-1999	99US-0144632
PR	20-JUL-1999	99US-0144684
PR	21-JUL-1999	99US-0144814
PR	21-JUL-1999	99US-0145086
PR	22-JUL-1999	99US-0145088
PR	22-JUL-1999	99US-0145089
PR	22-JUL-1999	99US-0145097
PR	22-JUL-1999	99US-0145192
PR	23-JUL-1999	99US-0145313
PR	23-JUL-1999	99US-0145324
PR	26-JUL-1999	99US-0145216
PR	27-JUL-1999	99US-0145913
PR	27-JUL-1999	99US-0145918
PR	28-JUL-1999	99US-0145951
PR	02-AUG-1999	99US-0146386
PR	02-AUG-1999	99US-0146388
PR	03-AUG-1999	99US-0147038
PR	04-AUG-1999	99US-0147204
PR	04-AUG-1999	99US-0147302
PR	05-AUG-1999	99US-0147192
PR	06-AUG-1999	99US-0147303
PR	06-AUG-1999	99US-0147416
PR	09-AUG-1999	99US-0147493
PR	09-AUG-1999	99US-0147935
PR	11-AUG-1999	99US-0148371
PR	11-AUG-1999	99US-0148319
PR	12-AUG-1999	99US-0148319
PR	13-AUG-1999	99US-0148565
PR	16-AUG-1999	99US-0149368
PR	17-AUG-1999	99US-0149175
PR	18-AUG-1999	99US-0149426
PR	20-AUG-1999	99US-0149722
PR	20-AUG-1999	99US-0149723
PR	20-AUG-1999	99US-0149929
PR	22-AUG-1999	99US-0149902
PR	23-AUG-1999	99US-0150066
PR	25-AUG-1999	99US-0150566
PR	27-AUG-1999	99US-0150684
PR	27-AUG-1999	99US-0151065
PR	27-AUG-1999	99US-0151067
PR	27-AUG-1999	99US-0151080
PR	30-AUG-1999	99US-0151103
PR	01-SEP-1999	99US-0151438
PR	07-SEP-1999	99US-0152363
PR	10-SEP-1999	99US-0153070
PR	13-SEP-1999	99US-0153758
PR	15-SEP-1999	99US-0154018
PR	16-SEP-1999	99US-0154779
PR	20-SEP-1999	99US-0155139
PR	22-SEP-1999	99US-0155485
PR	23-SEP-1999	99US-0155659
PR	24-SEP-1999	99US-0156458
PR	26-SEP-1999	99US-0156536
PR	04-OCT-1999	99US-0157117
PR	04-OCT-1999	99US-0157753
PR	06-OCT-1999	99US-0158029
PR	07-OCT-1999	99US-0158232
PR	08-OCT	

Query MatchConsistency 30.9%; Score 609.5; DB 21; Length 349;  
Best Local Similarity 38.9%; Pred. No. 8,9e-53;  
Matches 146; Conservative 70; Mismatches 122; Indels 37; Gaps 12;

9 MNEGSDGVSXKNAAS-YNIAIAKVPPEOCIRELIRANPINNICIRVADLGGASGPN 67  
1 meggdgansysaansrirkkvismakpvrivrtteamm-mtl-dtopykivaalgssgqs 58  
68 LITVDDIYQSIDKQGE-EKNELEPRTQIQLNDLRONDFNSYFKLLSEFRKLEKNGR 126  
59 flalelelncrlvncqvnms---peldccindpndntctfkrvfpfncelmitnk- 114  
127 KIGCSLIAMMGSTYGRHLPEESMHFLHSCYSVHMVSQVPSGLVIELGANKKSTYSSK 186  
115 --scctvvgagpsystslsrnslnhlnssayalmskvpckl-----enknlylts 166  
187 GCRPVQKAVLYDQFTKDFTPFLIRHSELFSRGMMLTLCICKVDEDEPNLD-----L 240  
167 sspgsayayaylngqkdfmflrlrseelvangrmvltflgr-nlndpilydcchfvl 225  
241 LDMATNDLIVGLLEBEKLDSPNIPFTPSAEKVCIVEBEGSCETLYLEFF--KAHYD 297  
226 lnsrldrlvfglvseskldafmpfydpnvqelkevlgkgsfeinleahgfdlghyy 285  
298 AAFSIDDDPYPRSHQCKAEYVASLIRSVYPTIFASHFGAIVPDLFRLKAKHAAYLHM 357  
286 e-----edfdeegne-----angravrsepmiahfgeelldtfdkyhyvtganc 334  
358 GKGCCYNLIISLAKK 372  
335 rnkltvsivalttk 349

RESULT 10  
AAIG2668  
ID AAIG2668 standard; protein: 327 AA.  
XX  
XX AAIG2668;  
XX  
XX 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 11899;  
KV Protein identification; signal transduction pathway; metabolic pathway;  
KV hybridisation assay; genetic mapping; gene expression control; promoter;  
KV termination sequence.  
XX  
OS Arabidopsis thaliana.  
PN EP1033405-A2.  
XX  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
EX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130440.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130691.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.



PR	22-JUL-1999	99US-0145089	PR	21-OCT-1999	99US-0160770
PR	22-JUL-1999	99US-0145089	PR	21-OCT-1999	99US-0160814
PR	22-JUL-1999	99US-0145192	PR	21-OCT-1999	99US-0160815
PR	22-JUL-1999	99US-0145192	PR	22-OCT-1999	99US-0160980
PR	23-JUL-1999	99US-0145218	PR	22-OCT-1999	99US-0160981
PR	23-JUL-1999	99US-0145224	PR	22-OCT-1999	99US-0160989
PR	25-JUL-1999	99US-0145276	PR	25-OCT-1999	99US-0161404
PR	27-JUL-1999	99US-0145313	PR	25-OCT-1999	99US-0161405
PR	27-JUL-1999	99US-0145318	PR	25-OCT-1999	99US-0161406
PR	28-JUL-1999	99US-0145391	PR	26-OCT-1999	99US-0161359
PR	02-AUG-1999	99US-0146386	PR	26-OCT-1999	99US-0161360
PR	02-AUG-1999	99US-0146388	PR	28-OCT-1999	99US-0161920
PR	03-AUG-1999	99US-0146389	PR	28-OCT-1999	99US-0161992
PR	04-AUG-1999	99US-0147038	PR	28-OCT-1999	99US-0161993
PR	04-AUG-1999	99US-0147204	PR	29-OCT-1999	99US-0162142
PR	05-AUG-1999	99US-0147192			
PR	05-AUG-1999	99US-0147260			
PR	06-AUG-1999	99US-0147303			
PR	06-AUG-1999	99US-0147416			
PR	09-AUG-1999	99US-0147493			
PR	09-AUG-1999	99US-0147935			
PR	10-AUG-1999	99US-0148171			
PR	11-AUG-1999	99US-0148319			
PR	13-AUG-1999	99US-0148341			
PR	13-AUG-1999	99US-0148565			
PR	13-AUG-1999	99US-0148684			
PR	16-AUG-1999	99US-0149368			
PR	17-AUG-1999	99US-0149175			
PR	18-AUG-1999	99US-0149432			
PR	20-AUG-1999	99US-0149722			
PR	20-AUG-1999	99US-0149723			
PR	20-AUG-1999	99US-0149723			
PR	23-AUG-1999	99US-0149902			
PR	23-AUG-1999	99US-0149920			
PR	23-AUG-1999	99US-0149930			
PR	25-AUG-1999	99US-0150566			
PR	25-AUG-1999	99US-0150884			
PR	27-AUG-1999	99US-0151066			
PR	27-AUG-1999	99US-0151080			
PR	30-AUG-1999	99US-0151303			
PR	31-AUG-1999	99US-0151438			
PR	01-SEP-1999	99US-0151930			
PR	07-SEP-1999	99US-0152363			
PR	10-SEP-1999	99US-0153070			
PR	13-SEP-1999	99US-0153758			
PR	15-SEP-1999	99US-0154018			
PR	16-SEP-1999	99US-0154039			
PR	20-SEP-1999	99US-0154779			
PR	22-SEP-1999	99US-0155139			
PR	23-SEP-1999	99US-0155486			
PR	24-SEP-1999	99US-0155659			
PR	28-SEP-1999	99US-0156456			
PR	29-SEP-1999	99US-0156596			
PR	04-OCT-1999	99US-0157117			
PR	05-OCT-1999	99US-0157753			
PR	06-OCT-1999	99US-0157865			
PR	07-OCT-1999	99US-0158022			
PR	12-OCT-1999	99US-0158232			
PR	12-OCT-1999	99US-0158365			
PR	13-OCT-1999	99US-0158293			
PR	13-OCT-1999	99US-0158294			
PR	14-OCT-1999	99US-0158329			
PR	14-OCT-1999	99US-0158330			
PR	14-OCT-1999	99US-0158331			
PR	14-OCT-1999	99US-0158637			
PR	18-OCT-1999	99US-0159584			
PR	21-OCT-1999	99US-0160741			
PR	21-OCT-1999	99US-0160767			
PR	21-OCT-1999	99US-0160768	</		

PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 04-MAY-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0134252.  
PR 14-MAY-1999; 99US-0134518.  
PR 14-MAY-1999; 99US-0134519.  
PR 14-MAY-1999; 99US-0134521.  
PR 14-MAY-1999; 99US-0134770.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137528.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 14-JUN-1999; 99US-0138847.  
PR 16-JUN-1999; 99US-0139319.  
PR 16-JUN-1999; 99US-0139432.  
PR 17-JUN-1999; 99US-0139453.  
PR 18-JUN-1999; 99US-0139453.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 21-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 08-JUL-1999; 99US-0142390.  
PR 09-JUL-1999; 99US-0142803.  
PR 12-JUL-1999; 99US-0142820.  
PR 13-JUL-1999; 99US-0142877.  
PR 13-JUL-1999; 99US-0143342.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144332.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 26-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0146389.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147182.  
PR 06-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 09-AUG-1999; 99US-0147463.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 16-AUG-1999; 99US-0148684.  
PR 17-AUG-1999; 99US-0149368.  
PR 18-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149920.  
PR 23-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151085.  
PR 27-AUG-1999; 99US-0151086.  
PR 27-AUG-1999; 99US-0151086.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155132.  
PR 22-SEP-1999; 99US-0155486.  
PR 28-SEP-1999; 99US-0156639.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.

PR 12-OCT-1999; 99US-0158369  
 PR 13-OCT-1999; 99US-0159293  
 PR 13-OCT-1999; 99US-0159294  
 PR 13-OCT-1999; 99US-0159295  
 PR 14-OCT-1999; 99US-0159329  
 PR 14-OCT-1999; 99US-0159330  
 PR 14-OCT-1999; 99US-0159331  
 PR 14-OCT-1999; 99US-0159637  
 PR 14-OCT-1999; 99US-0159638  
 PR 18-OCT-1999; 99US-0159584  
 PR 21-OCT-1999; 99US-0160741  
 PR 21-OCT-1999; 99US-0160767  
 PR 21-OCT-1999; 99US-0160770  
 PR 21-OCT-1999; 99US-0160814  
 PR 21-OCT-1999; 99US-0160815  
 PR 22-OCT-1999; 99US-0160980  
 PR 22-OCT-1999; 99US-0160981  
 PR 22-OCT-1999; 99US-0160989  
 PR 25-OCT-1999; 99US-0161404  
 PR 25-OCT-1999; 99US-0161405  
 PR 25-OCT-1999; 99US-0161406  
 PR 26-OCT-1999; 99US-0161359  
 PR 26-OCT-1999; 99US-0161360  
 PR 26-OCT-1999; 99US-0161361  
 PR 28-OCT-1999; 99US-0161920  
 PR 28-OCT-1999; 99US-0161992  
 PR 28-OCT-1999; 99US-0161993  
 PR 29-OCT-1999; 99US-0162142

Query Match 29.7%; Score 586; DB 21; Length 327;  
 Best Local Similarity 39.6%; Pred. No. 1.9e-50;  
 Matches 139; Conservative 65; Mismatches 111; Indels 36; Gaps 11;

OY 32 KPFEQCIKRLRANPNINCKIVADIGCASGPNLTVRDIQVSDIKVQOE-EKNELE 90  
 DB 3 kpylvnteeamm-mml-dfpcylkvaelgcsagqsfnlalfelntlvnlgqhknks-- 58  
 OY 91 RPTQIFLNDLONPNFNSFKLEKFKLEKGRKISGLISAMPSPFGRLPPEESM 150  
 DB 59 -peldecindpndntfctfivfnkelmtck---scsfvypapsfysrlfsmnl 114  
 OY 151 HFLHSGYVHMLSOVPSGLVELGIGANKSGISYSGKCRPVOKAYLDQFTKDTTLRI 210  
 DB 115 hlmsayalhwlskypckl-----enknqlyltspspsakaylnqfdtftmflr 168  
 OY 211 HSKELFSRGRMLTLCICKVDEDFDEPNPLD-----LIDMAINDLIVEGILEBEKLDSENI 264  
 DB 169 rseelvsngmvtlffigr-ntlndplyrdchfwllsmnelldlvfegivseskldafnm 227  
 OY 265 PFMPSAEVKKCIEREESCELYLEFP---KAHYDAASIDDDYVNSHEDIKAEVYAS 321  
 DB 228 pfygpnvgeikvckegsfelnelesngfdlghye-----eddfagagne-----an 276  
 OY 322 LIRSVYEPILASHFGALMPDLFRLAKHAKAYVLMKGGCYNLLISLAKK 372  
 DB 277 glravsepmlahfgeelidctfdckayhvtqancrntctvsilvsltkk 327

RESULT 12  
 ID AAG06670 standard; Protein; 374 AA.  
 AC AAG06670;  
 XX AAG06670;  
 DT 17-OCT-2000 (first entry)  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 3527.  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX

OS Arabidopsis thaliana.  
 XX EPI033405-A2.  
 PN  
 XX 06-SEP-2000.  
 PD  
 XX  
 XX 25-FEB-2000; 2000EP-0301439.  
 PF  
 XX 25-FEB-1999; 99US-0121825.  
 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123184.  
 PR 23-MAR-1999; 99US-0125788.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
 PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.  
 PR 08-APR-1999; 99US-0128714.  
 PR 16-APR-1999; 99US-0129845.  
 PR 19-APR-1999; 99US-0130077.  
 PR 21-APR-1999; 99US-0130049.  
 PR 23-APR-1999; 99US-0130510.  
 PR 23-APR-1999; 99US-0130891.  
 PR 28-APR-1999; 99US-0131848.  
 PR 30-APR-1999; 99US-0132407.  
 PR 04-MAY-1999; 99US-0132484.  
 PR 05-MAY-1999; 99US-0132485.  
 PR 06-MAY-1999; 99US-0132486.  
 PR 06-MAY-1999; 99US-0132487.  
 PR 07-MAY-1999; 99US-0132863.  
 PR 11-MAY-1999; 99US-0134256.  
 PR 14-MAY-1999; 99US-0134218.  
 PR 14-MAY-1999; 99US-0134219.  
 PR 14-MAY-1999; 99US-0134221.  
 PR 14-MAY-1999; 99US-0134370.  
 PR 18-MAY-1999; 99US-0134768.  
 PR 19-MAY-1999; 99US-0134941.  
 PR 20-MAY-1999; 99US-0135124.  
 PR 21-MAY-1999; 99US-0135353.  
 PR 24-MAY-1999; 99US-0135629.  
 PR 25-MAY-1999; 99US-0135621.  
 PR 27-MAY-1999; 99US-0135632.  
 PR 28-MAY-1999; 99US-0135782.  
 PR 01-JUN-1999; 99US-0137222.  
 PR 03-JUN-1999; 99US-0137528.  
 PR 04-JUN-1999; 99US-0137502.  
 PR 07-JUN-1999; 99US-0137724.  
 PR 08-JUN-1999; 99US-0138094.  
 PR 10-JUN-1999; 99US-0138540.  
 PR 10-JUN-1999; 99US-0138847.  
 PR 14-JUN-1999; 99US-0139119.  
 PR 16-JUN-1999; 99US-0139452.  
 PR 16-JUN-1999; 99US-0139453.  
 PR 17-JUN-1999; 99US-0139492.  
 PR 18-JUN-1999; 99US-0139454.  
 PR 18-JUN-1999; 99US-0139455.  
 PR 18-JUN-1999; 99US-0139456.  
 PR 18-JUN-1999; 99US-0139457.  
 PR 18-JUN-1999; 99US-0139458.  
 PR 18-JUN-1999; 99US-0139459.  
 PR 18-JUN-1999; 99US-0139460.  
 PR 18-JUN-1999; 99US-0139461.  
 PR 18-JUN-1999; 99US-0139462.  
 PR 18-JUN-1999; 99US-0139463.  
 PR 18-JUN-1999; 99US-0139750.  
 PR 18-JUN-1999; 99US-0139763.  
 PR 21-JUN-1999; 99US-0139817.  
 PR 22-JUN-1999; 99US-0139819.  
 PR 23-JUN-1999; 99US-0140353.  
 PR 23-JUN-1999; 99US-0140354.  
 PR 24-JUN-1999; 99US-0140625.  
 PR 28-JUN-1999; 99US-0140823.  
 PR 29-JUN-1999; 99US-0140991.



Db 343 lfavestratshakv1 359

RESULT 13

AG46653 standard; Protein: 374 AA.

XX AG46653;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 58716.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridization assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS Epi033405-A2.

PV 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439;

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0133256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135355.

PR 24-MAY-1999; 99US-0135628.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139455.

PR 16-JUN-1999; 99US-0139455.

PR 17-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 02-JUL-1999; 99US-0142154.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142820.

PR 12-JUL-1999; 99US-0142877.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143524.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145088.

PR 21-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145098.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 26-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 03-AUG-1999; 99US-0146389.

PR 04-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147935.

PR 09-AUG-1999; 99US-0148171.

PR 10-AUG-1999; 99US-0148319.

PR 11-AUG-1999; 99US-0148341.

PR 12-AUG-1999; 99US-0148341.

PR 13-AUG-1999; 99US-0148345.

PR 13-AUG-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.

PR 17-AUG-1999; 99US-0149175.

PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151080.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 23-OCT-1999; 99US-0161404.  
PR 23-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161922.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.  
Query Match 21.9%; Score 432; DB 21; Length 374;  
Best Local Similarity 32.6%; Pred No. 8e-35;  
Matches 123; Conservative 55; Mismatches 159; Indels 40; Gaps 11;

QY 1 MELQVLEHNEGDDTAYANASYINLAKVPEFEOCIRFLNANLPIN-----KC 53  
DB 1 mkterlismkqgkqgdsyamsqamhar-----smlllleclenvhlnssasppp 53  
QY 54 IKVADIGASGPNLTIVROIVOSIDKVGQEEKNELERPTIOIFLNDLFQNDNSVFKIL 113  
DB 54 ftevdvgssgnentlvhidivkhik--rfdaagidppetfatfsdipendfnllfql 111  
QY 114 PSFYRLERKE-----NGRKIGSCLISAMPGSFYGRLLFPEESMHLHSCYSVHWLSCVPSG 168

DB 112 pvlsvntcmeeclaadgnr--syfvagvpsfyrllfpartldffhsafshwlsqyps 169  
QY 169 LVELLEIGANKSISYSGKCRPVOQKAYLDQFKDPTFLRHSEKLEPSNGRMILCTI-- 226  
DB 170 vctirraaynrgvrf-Ingasektcttckrgfgadlaeellraraevrggamflvcldgr 228  
QY 227 CKYDERDEPNPLDLDLDM-----AINDLVEGLEEERKLDPSFNPFPTPAEVCYIEEG 282  
DB 229 tsydpdcaggagllfctgfqadwddlvreglvaaekrdgfnipyapslqofkevdaang 288  
QY 283 SCEILYLETFKKAHYDAFSDIDYVRSRQIAEYVASLRSYVEPTLASHREGAIMPD 342  
DB 289 sfldklivvykxgspdlvnpedq-----asevgra--faascrsyagvlveahigeelsnk 342  
QY 343 LFRHL-----AKHAKVL 355  
DB 343 lfavestratshakavl 359  
RESULT 14  
AAG06669 standard; Protein; 386 AA.  
ID AAG06669  
AC AAG06669;  
XX 17-OCT-2000 (first entry)  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3526.  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridization assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS EPI033405-A2.  
PN XX  
XX 06-SEP-2000.  
PD XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 29-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 05-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138340.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139432.  
PR 17-JUN-1999; 99US-0139432.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139897.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140635.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143634.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144086.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144335.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 21-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 23-JUL-1999; 99US-0145112.  
PR 23-JUL-1999; 99US-0145115.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147204.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148314.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151302.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0155479.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158123.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.

PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.  
Query Match 21.9%; Score 432; DB 21; Length 386;  
Best Local Similarity 32.6%; Pred. No 8.3e-35;  
Matches 123; Conservative 55; Mismatches 159; Indels 40; Gaps 11;  
OY 1 MELQGLVHANEGBDTSYAKNKNSTYLAALAKYKPLEOCIEHLEIRANLPIN-----KC 53  
DB 13 mKlerlismkgqygqdsyannsqamhar-----smhlleclenhnssasppp 65  
OY 54 IKVADLGASCPMTLLTVRDIVQSIDKVGQEKNELEPTIQFLNDLPONDPSVFKLL 113  
DB 66 fctvcdgssgsantvhlidflvkhsK--rtdaagldppeftafadlpsndfnlfgll 123  
OY 114 pSFYKLEKE-----NQRKISCLISAMPGSFYGRLPPEESMHFLSCYSVHMLSOVPSG 168  
DB 124 plviantcmeciaadgnr--syfvaqvgafyrrllpartldffhsatshlwspes 181  
OY 169 LVIEELGICANGSTYSKCGRPVOKAYLDQFTPTPRIRIKSELPFRGHMLTCT-- 226  
DB 182 vdrtsaayngarf-lhgagckttaykrqfagdlaeflrataaevkrgamflvcigr 240  
OY 227 CVYDEFEDEPNLDLDMK---ANDLIYEGLEBEKLDSENFIPFPSPAEVKCYEEEG 282  
DB 241 tsvcdcdgsgagllfcthdadadlvreglvaaektdgfnlpybpsldqdkvvdang 300  
OY 283 SCEITLYLTFFAHTDAAFSIDDDYPRSHBOIKAEVYASLRSYIEPIIASHFGEALMPD 342  
DB 301 staklklvvygsgplvneppd---asevgra--fascrcvavglveahlgaelank 354  
OY 343 LFHRL---ANHAAKVL 355  
DB 355 llsrvesratshakvdl 371  
RESULT 15  
AA646652  
ID AA646652 standard; Protein; 386 AA.  
AC AA646652;  
XX 18-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SPO ID NO: 58715.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PE 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
XX PR 05-MAR-1999; 99US-0123180.  
XX PR 09-MAR-1999; 99US-0123548.  
XX PR 23-MAR-1999; 99US-0123788.  
XX PR 23-MAR-1999; 99US-0126264.  
XX PR 29-MAR-1999; 99US-0126785.  
XX PR 01-APR-1999; 99US-0127462.  
XX PR 08-APR-1999; 99US-0128334.  
XX PR 16-APR-1999; 99US-0129845.  
XX PR 19-APR-1999; 99US-0130077.  
XX PR 21-APR-1999; 99US-0130449.  
XX PR 23-APR-1999; 99US-0130510.  
XX PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134700.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 25-MAY-1999; 99US-0135629.  
PR 27-MAY-1999; 99US-0136021.  
PR 28-MAY-1999; 99US-0136392.  
PR 01-JUN-1999; 99US-0136782.  
PR 03-JUN-1999; 99US-0137222.  
PR 04-JUN-1999; 99US-0137528.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 14-JUN-1999; 99US-0138847.  
PR 16-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 17-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139889.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140685.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 08-JUL-1999; 99US-0142390.  
PR 09-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 14-JUL-1999; 99US-0143562.  
PR 14-JUL-1999; 99US-0143654.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 16-JUL-1999; 99US-0144385.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.





---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2002, 04:40:49 ; Search time 19.54 Seconds  
(without alignments)  
472.511 Million cell updates/sec

Title: US-09-971-020-1

Sequence: 1 MRLQVLMHNGEDTSTYAR.....KCCYNMLIISLAKPKESDV 378

Scoring table: BLOSUM62

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCtus\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfillseq1.pep:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	4.8	707	1 US-08-528-122-18	Sequence 18, Appl
2	94	4.8	707	5 PCT-US95-11720-18	Sequence 18, Appl
3	94	4.8	750	1 US-08-325-553-2	Sequence 2, Appl
4	94	4.8	750	2 US-08-394-152A-2	Sequence 2, Appl
5	94	4.8	750	4 US-09-044-668-2	Sequence 2, Appl
6	91.5	4.6	1854	4 US-09-004-838-108	Sequence 108, App
7	89	4.5	475	4 US-09-009-494-6	Sequence 6, Appl
8	89	4.5	475	4 US-09-010-233-2	Sequence 2, Appl
9	89	4.5	475	4 US-09-010-233-6	Sequence 6, Appl
10	87	4.4	857	2 US-08-779-113-2	Sequence 2, Appl
11	87	4.4	856	2 US-08-583-562B-2	Sequence 2, Appl
12	86.5	4.4	442	1 US-08-363-255-1	Sequence 4, Appl
13	86.5	4.4	442	1 US-08-363-255-1	Sequence 11, Appl
14	86.5	4.4	442	1 US-08-363-255-1	Sequence 43, Appl
15	85.5	4.3	445	1 US-08-363-255-1	Sequence 5, Appl
16	85.5	4.3	445	1 US-08-363-255-1	Sequence 12, Appl
17	85	4.3	756	4 US-09-085-199B-9	Sequence 9, Appl
18	85	4.3	2161	3 US-09-081-320-3	Sequence 3, Appl
19	84.5	4.3	1140	4 US-09-651-655-21	Sequence 21, Appl
20	84.5	4.3	3218	4 US-08-764-100-27	Sequence 27, Appl
21	84	4.3	636	4 US-09-564-805-237	Sequence 16, Appl
22	83.5	4.2	166	1 US-08-362-453-16	Sequence 16, Appl
23	83.5	4.2	560	3 US-09-176-657-7	Sequence 20, Appl
24	83	4.2	900	1 US-08-425-061-20	Sequence 20, Appl
25	83	4.2	900	3 US-08-825-886-20	Sequence 20, Appl
26	83	4.2	914	1 US-08-425-061-21	Sequence 21, Appl
27	83	4.2	914	2 US-08-825-886-21	Sequence 21, Appl

28	83	4.2	1202	1 US-08-425-061-22	Sequence 22, Appl
29	83	4.2	1202	2 US-08-825-886-22	Sequence 22, Appl
30	83	4.2	1363	1 US-08-425-061-23	Sequence 23, Appl
31	83	4.2	1363	2 US-08-825-886-23	Sequence 23, Appl
32	83	4.2	1852	1 US-08-425-061-24	Sequence 24, Appl
33	83	4.2	1852	2 US-08-825-886-24	Sequence 24, Appl
34	83	4.2	1863	1 US-08-425-061-16	Sequence 16, Appl
35	83	4.2	1863	1 US-08-480-784-2	Sequence 2, Appl
36	83	4.2	1863	1 US-08-483-553-2	Sequence 2, Appl
37	83	4.2	1863	1 US-08-487-002-2	Sequence 2, Appl
38	83	4.2	1863	1 US-08-483-554B-2	Sequence 2, Appl
39	83	4.2	1863	1 US-08-488-011B-2	Sequence 2, Appl
40	83	4.2	1863	1 US-08-825-886-16	Sequence 16, Appl
41	83	4.2	1863	2 US-08-603-753D-2	Sequence 2, Appl
42	83	4.2	1863	4 US-09-099-753-2	Sequence 2, Appl
43	83	4.2	1863	4 US-08-850-727-2	Sequence 2, Appl
44	83	4.2	1863	4 US-08-986-106-2	Sequence 2, Appl
45	83	4.2	1863	4 US-09-007-678B-49	Sequence 49, Appl

## ALIGNMENTS

RESULT 1  
US-08-528-122-18  
Sequence 18, Application US/08528122  
Patent No. 5726044  
GENERAL INFORMATION:  
APPLICANT: LO, KIM-MING  
APPLICANT: SUDO, YUKIO  
TITLE OF INVENTION: GILLES, STEPHEN D.  
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
ADDRESS: THIBEAULT  
STREET: 125 HIGH STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/528,122  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER, EDMUND R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: FIP-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 707 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/key: Protein  
LOCATION: 1..707  
OTHER INFORMATION: /note="EXTRACELLULAR DOMAIN OF  
OTHER INFORMATION: PSMA"  
US-08-528-122-18

Query Match 4.8%; Score 94; DB 1; Length 707;  
Best Local Similarity 24.8%; Pred. No. 0.24;  
Matches 53; Conservative 24; Mismatches 61; Indels 76; Gaps 13

Y 154 HSGSYVHML-----SOVPSGVITELGIGANK-----G 180  
D 510 HAYETIETELVERKEFIDPMEKHYHLVAQVRGNATPEL---ANSIVLPDCDAVAVLRKYAD 566  
O 181 STYSKGRPRPVQAKAAYLDOTKFT----TELRHSKLSRGMALLTICAKYDFEDPNP 237  
Db 567 KITSISMAKHPOEMKTYSVSFDLSFKVNKFELASK--ESE-----RIODFSNP 615  
O 238 LDLLDMAINDILIVEGLLEEKLDSFNIP-----FFTSAEVKCIYEERGSCETLYL 289  
Db 616 IYLRRM--NDOLM--FLERAFIDPLGLPDPRPHRYHVAPSSHN-----KVAG----- 659  
O 290 EEFKAHYDAFSDIDDY-PVRSHEQIKAE-YVAS 321  
Db 660 ESFPGIYDALFDIESKYDPSPKAGEVKROIYVA 693

RESULT 2  
PCT-US95-11720-18  
Sequence 18, Application PC/TUS9511720  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HORWITZ &  
ADDRESS: THIBEAULT  
STREET: 125 HIGH STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIA TYPE: FLOPPY disk.  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/11720  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER, EDMUND R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: FIP-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 707 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..707  
OTHER INFORMATION: /note= "EXTRACELLULAR DOMAIN OF  
OTHER INFORMATION: PSMA"  
PCT-US95-11720-18

Query Match 4.8%; Score 94; DB 5; Length 707;  
Best Local Similarity 24.8%; Pred. No. 0.24;  
Matches 53; Conservative 24; Mismatches 61; Indels 76; Gaps 13

Y 154 HSGSYVHML-----SOVPSGVITELGIGANK-----G 180

```

Db      510 HAVETVLEAEKFDPEMKYHLTVAGNGVFTEL---ANSIVLFFDCRDYAVYLRYAD    566
Oy      181 SYSSKGRPRPVOKAYILDQFTDFT---TELRHSKELSRGMILLTICKVEFDEPNP    237
Db      567 KITSISKHNPDKMTTSVSFDSLFAVNKFELASK--FSE-----RLDQFKSNP     615
Oy      238 LIDLMAINDIIVEGLLEEKLDSFNIP-----FTTPSAEKCIVEEGSCITLYL    289
Db      616 IYLRNM--NDOLM--FLERAFIDPLGDRPFYRHVYAPSSHN-----KYAG-----    659
Oy      290 ETFKAHYDAFSIDDY-PYRSHEQINAE-YVAS    321
Db      660 ESFPDIYDALDIESKYDPSKAMGEVKROIYVA    693

RESULT          3
US-08-325-553-2
; Sequence 2, Application US/08325553
; Patent No. 553866
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heslon, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325.553
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973.337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-325-553-2

Query Match          4.8%; Score 94; DB 1; Length 750;
Best Local Similarity 24.8%; Pred. No. 0.26;
Matches 53; Conservative 24; Mismatches 61; Indels 76; Gaps 13;

Oy      181 SYSSKGRPRPVOKAYILDQFTDFT---TELRHSKELSRGMILLTICKVEFDEPNP    237
Db      610 KITSISKHNPDKMTTSVSFDSLFAVNKFELASK--FSE-----RLDQFKSNP     658

```

DB 238 LDLLDMAINDLVEGLLEBEKIDSFNIP-----FFPSAEVKCIYEESGCEILYL 289  
DB 659 IYLRMM--NDQLM--FLERAFIDPLGLDPRFYRHVIYAPSSHN-----KYAG-----702  
QY 290 EYFKAHYDAFASIDDDY-PVRSHEQIKAE-YYAS 321  
DB 703 ESFPGLIYDALFDIESKVDPSKAMGEVYKROIYYAA 736

RESULT 4  
US-08-394-152A-2  
Sequence 2, Application US/08394152A  
Patent No. 5935818  
GENERAL INFORMATION:  
APPLICANT: Isreali, Ron S.  
APPLICANT: Heston, Warren D.W.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESS: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 330 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,152A  
FILING DATE: 24-FEB-95  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41426-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 750 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-394-152A-2

Query Match 4.8%; Score 94; DB 2; Length 750;  
Best Local Similarity 24.8%; Pred. No. 0.26;  
Matches 53; Conservative 24; Mismatches 61; Indels 76; Gaps 13;

QY 154 HSCYSVHML-----SOVPSGLVLEIGIGANK-----G 180  
DB 553 HSYVYTYLVEKEFYDPMKYHLVAOVROGAVFEL---ANSIVLPFCRDYAVVLYKXAD 609  
QY 181 SYSSKGRPRPVQKAYLDQFTKDF---TFLRIHSKELFSRGRMLTLCICKYDEDEPNP 237  
DB 610 KIYSISMHPQEMKTYVSFDSLSAVKNFTELASK--FSE-----RLDDFKSNP 658  
QY 238 LDLLDMAINDLVEGLLEBEKIDSFNIP-----FFPSAEVKCIYEESGCEILYL 289  
DB 659 IYLRMM--NDQLM--FLERAFIDPLGLDPRFYRHVIYAPSSHN-----KYAG-----702  
QY 290 EYFKAHYDAFASIDDDY-PVRSHEQIKAE-YYAS 321  
DB 703 ESFPGLIYDALFDIESKVDPSKAMGEVYKROIYYAA 736

RESULT 5  
US-09-044-668-2  
Sequence 2, Application US/09044668  
Patent No. 6150508  
GENERAL INFORMATION:  
APPLICANT: Murphy, Gerald P.  
APPLICANT: Holmes, Eric H.  
APPLICANT: Boynton, Alton L.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC  
TITLE OF INVENTION: FOR THE EXTRACELLULAR DOMAIN OF PROSTATE-SPECIFIC  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/044,668  
FILING DATE: 18-MAR-1998  
CLASSIFICATION: 536  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Baldwin, Geraldine F.  
REGISTRATION NUMBER: 31,232  
REFERENCE/DOCKET NUMBER: 8511-0013-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 750 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6150508e  
US-09-044-668-2

Query Match 4.8%; Score 94; DB 4; Length 750;  
Best Local Similarity 24.8%; Pred. No. 0.26;  
Matches 53; Conservative 24; Mismatches 61; Indels 76; Gaps 13;

QY 154 HSCYSVHML-----SOVPSGLVLEIGIGANK-----G 180  
DB 553 HSYVYTYLVEKEFYDPMKYHLVAOVROGAVFEL---ANSIVLPFCRDYAVVLYKXAD 609  
QY 181 SYSSKGRPRPVQKAYLDQFTKDF---TFLRIHSKELFSRGRMLTLCICKYDEDEPNP 237  
DB 610 KIYSISMHPQEMKTYVSFDSLSAVKNFTELASK--FSE-----RLDDFKSNP 658  
QY 238 LDLLDMAINDLVEGLLEBEKIDSFNIP-----FFPSAEVKCIYEESGCEILYL 289  
DB 659 IYLRMM--NDQLM--FLERAFIDPLGLDPRFYRHVIYAPSSHN-----KYAG-----702  
QY 290 EYFKAHYDAFASIDDDY-PVRSHEQIKAE-YYAS 321  
DB 703 ESFPGLIYDALFDIESKVDPSKAMGEVYKROIYYAA 736

US-09-004-838-108  
Sequence 108, Application US/09004838  
Patent No. 6350933  
GENERAL INFORMATION:  
APPLICANT: Michelmore, Richard W.  
APPLICANT: Shen, Kathy  
APPLICANT: Meyers, Blake  
TITLE OF INVENTION: Procedures and Materials for  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk.  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,838  
FILING DATE: 09-JAN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/781,734  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmhorn, Gregory P.  
REGISTRATION/DOCKET NUMBER: 023070-078810US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ. ID NO.: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1854 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY:  
LOCATION: 1..1854  
OTHER INFORMATION: /note="RG2J deduced sequence"  
US-09-004-838-108

Query Match 4.6% Score 91.5; DB 4; Length 1854;  
Best Local Similarity 22.0%; Pred. No. 2.2; Mismatches 155; Indels 105; Gaps 27;  
Matches 92; Conservative 67;

QY 3 LOEVLHMEGEGDTSYAKNASTYMLAKVPELEOCIRELLANPININ-KCIKXVADG 60  
DB 820 MEELHRTGSEBGT-----TFPKLLKLLHGLPMLGLCL-VNNAIEPKLVOMK 869  
QY 61 CASGPN-TLLVTVDIVOSIDRVQGEKNELEPTTQIFINDLFONDENSVERKLLPSFYRK 119  
DB 870 LYSIPGTSITVRNKLKLSL-----KEEVVIRKIDI-----LEIHDMNKLKEIIPSELSR 921  
QY 120 LKENGKRI--GSC--LISAMPGSFYGRLLPERSMAFL-----SCYSVHMLQVPS 167  
DB 922 GEKVKRKIKVNRCKLVN-----LPPHNPMSLHLEBELIVEKSGSIEELFRIDI 972  
QY 168 GLVLELIGANKGS-----IYSKGC--RP-----PVQKAYL---DOFL 201  
DB 973 DCAVIGEEDNNSSLRNINVENSMKLRVWRKIGAGNSRPLRGVQVEKIIIRCKRFT 1032  
QY 202 KDFETFLIRHSELSRGRML-LTICK-VDPEDEPNPLDLDMAINDLYESGLEBEKI 259  
DB 1033 NVTFPI-----TTFNDGLALFLFISVDGRNDESDQNO-----EQDQIIELEKKTLDQERT 1083

QY 260 USF-NIPFTPSAEVVKCIVEEGSCCELLYLETFRKAHYDAEISIDDVYVNSHQIAEY 318  
DB 1084 DSIENVF--PS-----CLMHSFNLQKLLINRVKG-VEVVEIESESPT--SREIVYTHH 1134  
QY 319 VASLIRSYEPIPLASHFGGEAIPDLFHLAKAKVLMGKGCYN-NLISLAKPKES 376  
DB 1135 -----NQOQPV-----IPNLQHLIDLGMNDMIRVWK-CSNNKFFTLKQOSSS 1178

RESULT 7  
US-09-009-494-6  
Sequence 6, Application US/09009494  
Patent No. 6150340  
GENERAL INFORMATION:  
APPLICANT: Black, Michael T.  
APPLICANT: Lawlor, Elizabeth J.  
APPLICANT: Lewis, Carl J.  
TITLE OF INVENTION: No. 6150340el Compounds  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dechert, Price & Rhoads  
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2793  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,494  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/037,857  
FILING DATE: 07-FEB-1997  
APPLICATION NUMBER: 60/044,365  
FILING DATE: 28-APR-1997  
APPLICATION NUMBER: 60/044,366  
FILING DATE: 28-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Falk, Stephen T.  
REGISTRATION/DOCKET NUMBER: 36,795  
REFERENCE/DOCKET NUMBER: GM50028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-994-2488  
TELEFAX: 215-994-2222  
TELEX:  
INFORMATION FOR SEQ. ID NO.: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 475 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-009-494-6

Query Match 4.5% Score 89; DB 4; Length 475;  
Best Local Similarity 20.6%; Pred. No. 0.44;  
Matches 80; Conservative 63; Mismatches 160; Indels 86; Gaps 16;

QY 7 LHMNEGEGDTSYAKNASTYMLAKVPELEOCIRELLA-----NLPRINQICIVA 57  
DB 121 LHMEDAGKSTHNGEISLVDLNRQSTPLIEIVSEPDIRSPKEAVALEKLSIIQYGSV 180  
QY 58 DLGASGPNLLVR-DIVQSIDKQGE--KNLEPRPIQIFINDLFONDENSVERKLL 113  
DB 181 DVKMEG-----SLRCDANISIRPYGDEKFGTKNELNN-----LNSFIVYKGL 224  
QY 114 PSYRKLEK--NGRKIG-----SCLISAMPGSFYGRLLPERSM--HFLHSCY 157

Db 225 EYKRGEBELNGEIGQFRRPDESTGTILMRKESDDYRFFPPDVLPIYIDAM 284  
 QY 158 SVHMLSQVP-----SGLYELGIGANKSISYSSKGCRRPVQKAYLDOFTKFTPLRI 210  
 Db 285 KERVQRTITPELPERKAKYVNEGL-----PAYDAHVLTITKREMSDFES 329  
 QY 211 ---HSEKLEFSRGMILTCICVDFEPPNPLDLDMAINDLIVEGLE-----EKKLD 260  
 Db 330 TIEHGADVKTLSNMLMG---GVNEYLNKNQVVELDTPKLPENLAGMIKILIEDGTMSKIA 386  
 QY 261 SFNIPFTPSAEVCIYEESGCEILYEFKHAHYDAFISIDDPVPSHQKAEYVA 320  
 Db 387 KKVPELLAANGAKOIMEDNGLVQISDEATILTKFVNEALD--NNEQSVEDYKNGKGRAMG 445  
 QY 321 SLIRSYEPTILASHGEAIMPDLFHRLAK 349  
 Db 446 FLVQO-----IMKASKQA-NPOLVNOILK 469

## RESULT 8

US-09-010-233-2  
 ; Sequence 2, Application US/09010233  
 ; Patent No. 6200774

## GENERAL INFORMATION:

APPLICANT: Black, Michael T.  
 APPLICANT: Lawlor, Elizabeth J.  
 TITLE OF INVENTION: No. 6200774el Compounds  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert, Price & Rhoads  
 STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/010,233  
 FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/037,857  
 FILING DATE: 07-FEB-1997  
 APPLICATION NUMBER: 60/044,365  
 FILING DATE: 28-APR-1997  
 APPLICATION NUMBER: 60/044,366  
 FILING DATE: 28-APR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: Falk, Stephen T.  
 REGISTRATION NUMBER: 36,795  
 REFERENCE/DOCKET NUMBER: GMS0027  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-994-2488  
 TELEFAX: 215-994-2222

## TELEX:

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 475 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-09-010-233-2

Query Match 4.5%; Score 89; DB 4; Length 475;  
 Best Local Similarity 20.6%; Preg. No. 0.44;  
 Matches 80; Conservative 63; Mismatches 160; Indels 86; Gaps 16;

QY 7 LHMNEGDSYKASNYALAKYVPLEGCIPELLRA-----NLPINKCIKYVA 57  
 Db 121 LHMEDGKSTHNGEYSVLDNRGOTPLIEYSEPDIRSPKAYVALEKLSIIQYGVYS 180  
 QY 58 DLGASCPNMLTVR-DIVQSIDKYGQEE---KNELEPTIOLFINDLFQDNFYSVKLL 113  
 Db 191 DVKMEES---SLRQDANISLRPYGDEKRGTAELN-----LNSFYVAKGL 224  
 QY 114 PSFYKLEKE--NGRRIG-----SCLISAMPSEFYGRLPPEESN--HFLHSCY 157  
 Db 225 EYKRGEBELNGEIGQFRRPDESTGTILMRKESDDYRFFPPDVLPIYIDAM 284  
 QY 158 SVHMLSQVP-----SGLYELGIGANKSISYSSKGCRRPVQKAYLDOFTKFTPLRI 210  
 Db 285 KERVQRTITPELPERKAKYVNEGL-----PAYDAHVLTITKREMSDFES 329  
 QY 211 ---HSEKLEFSRGMILTCICVDFEPPNPLDLDMAINDLIVEGLE-----EKKLD 260  
 Db 330 TIEHGADVKTLSNMLMG---GVNEYLNKNQVVELDTPKLPENLAGMIKILIEDGTMSKIA 386  
 QY 261 SFNIPFTPSAEVCIYEESGCEILYEFKHAHYDAFISIDDPVPSHQKAEYVA 320  
 Db 387 KKVPELLAANGAKOIMEDNGLVQISDEATILTKFVNEALD--NNEQSVEDYKNGKGRAMG 445  
 QY 321 SLIRSYEPTILASHGEAIMPDLFHRLAK 349  
 Db 446 FLVQO-----IMKASKQA-NPOLVNOILK 469

## RESULT 9

US-09-010-232-6  
 ; Sequence 6, Application US/09010232  
 ; Patent No. 6248557

## GENERAL INFORMATION:

APPLICANT: Black, Michael T.  
 APPLICANT: Lawlor, Elizabeth J.  
 TITLE OF INVENTION: No. 6248557el Compounds  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert, Price & Rhoads  
 STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/010,232  
 FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/937,857  
 FILING DATE: 07-FEB-1997  
 APPLICATION NUMBER: 60/044,366  
 FILING DATE: 28-APR-1997  
 APPLICATION NUMBER: 60/044,365  
 FILING DATE: 28-APR-1997

## ATTORNEY/AGENT INFORMATION:

NAME: Falk, Stephen T.  
 REGISTRATION NUMBER: 36,795  
 REFERENCE/DOCKET NUMBER: GMS0026  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-994-2488  
 TELEFAX: 215-994-2222

## TELEX:

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-010-232-6

Query Match 4.54; Score 89; DB 4; Length 475;  
 Best Local Similarity 20.64; Pred. No. 0.44; Mismatches 160; Indels 86; Gaps 16;  
 Matches 80; Conservative 63;

DB 7 LHNNEGDTSTAKNANALAKVFPLEQCIKRELA-----NIPNKKCIKVA 57  
 DB 121 LHNNEGDTSTAKNANALAKVFPLEQCIKRELA-----NIPNKKCIKVA 180  
 OY 58 DLCCASGPTLLTVR-DIVOSIDKVGQEE--KNELEPPTIQIILNDLFONDENVFKLL 113  
 DB 181 DVMERG-----SLRCQANISLRPYQGEKFKRAELKN-----INSFNVRKGL 224  
 OY 114 PSFYRLKEE--NGRKIG-----SCLISAMPGSFYGRLPFEESM--HFLHSCY 157  
 DB 225 EYEERKQEBELNGEIQETRRFDESTGTILMRKKGSDDYRPEPDIYPLIIDAM 284  
 OY 158 SVHMLSQV-----SGLVIEIGIGANKSIIYSKGRPPYQKAYLDQFTKDTFFELRI 210  
 DB 285 KERVROTIELDEPKKAYVNEGL-----PAYDAHVLTITKMSDPFES 329  
 OY 211 ---HSEKLSRGRMLTICICVDEPDPNLDLMAINDLIVGLE-----BEKID 260  
 DB 330 TIRHGDVLTIRNMLG---GVNITLKNQVELDQKLPENLAGMKRLIEDGTMSKIA 386  
 OY 261 SFNIPFTPSAEVVCIVVEEGSCIIYLETFRKAYDAFSIDDPYVRSHQIKAEYVA 320  
 DB 387 KVFPEPLAKGNAQIMEDGLVQISDENTYLLKTFVNEALD--NNEQSEVDYKNGKKGAMG 445  
 OY 321 SLIRSYEPILASHGEAIMPDEHRLAK 349  
 DB 446 FLVGO---IMKASKGA--NFOVLNOLK 469

RESULT 10  
 US-08-779-113-2  
 Sequence 2, Application US/08779113  
 Patent No. 5948891  
 GENERAL INFORMATION:  
 APPLICANT: Staunton, Donald E.  
 APPLICANT: Harris, Edith S.  
 TITLE OF INVENTION: Cytoplasmic Modulators of Integrin  
 TITLE OF INVENTION: Binding  
 NUMBER OF SEQUENCES: 65  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 233 South Wacker Drive, 6300 Sears Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,113  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Greta E. No. 5948891and  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/33773  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 857 amino acids  
 TYPE: amino acid  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: protein  
 US-08-779-113-2

Query Match 4.48; Score 87; DB 2; Length 857;  
 Best Local Similarity 18.78; Pred. No. 1.9; Mismatches 60; Indels 54; Gaps 4;  
 Matches 31; Conservative 21;

OY 247 DLVIEGLEBEKLDSENPFTPSAEVVCIVVEEGSCIIYLETFRKAYDAFSIDDPY 306  
 DB 110 DLAEIG-----PSKAEISIDKNDGCTVTYLTPLPEDYSILVKYNDKH 153  
 OY 307 -----PVSRHQIKAEYVASLIRSYEPILAS----- 333  
 DB 154 IPGSPYAKITDSDSRCSQVTLGSAADFLDISETDLSLTFASIRAPSGRDEPCLRLP 213  
 OY 334 --HGEALIMPDLFHLRAKAAKVLHMKGCCYNNLIISLAKPKESD 377  
 DB 214 NNHGISFLP---REVGEHLVSIKKNGNHVAISPVSIMVQSEID 256

RESULT 11  
 US-08-583-562B-2  
 Sequence 2, Application US/08583562B  
 Patent No. 5922570  
 GENERAL INFORMATION:  
 APPLICANT: Staunton, Donald  
 APPLICANT: Harris, Edith  
 TITLE OF INVENTION: Cytoplasmic Modulators of Integrin  
 TITLE OF INVENTION: Binding  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 233 South Wacker Drive, 6300 Sears Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/583,562B  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: 38,659  
 REFERENCE/DOCKET NUMBER: 27866/33033  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 858 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-583-562B-2

Query Match 4.48; Score 87; DB 2; Length 858;  
 Best Local Similarity 18.78; Pred. No. 1.9; Mismatches 54; Gaps 4;  
 Matches 31; Conservative 21;

OY 247 DLVIEGLEBEKLDSENPFTPSAEVVCIVVEEGSCIIYLETFRKAYDAFSIDDPY 306



DB 110 DLAIEG-----PSKAEISCIKNDGCTCVTLPLPDYSLVKYNDKH 153  
OY 307 -----PVSHBQIKAEVYASLIRSYEPIAS----- 333  
DB 154 IPGSPFARKITDSDRSCGVKLSAOPFLDISPTDLSITLSIKAPSGRDEPCLLRP 213  
OY 334 --HGEKAMPDLFHLAKHAKVILHMGKGCYNLIISLAKPEKD 377  
DB 214 NNHIGISFIP---REVGEHLVSIKKNHNVANSFVSLMVOSIED 256

RESULT 12  
US-08-363-255-4  
Sequence 4, Application US/08363255  
Patent No. 5783386  
GENERAL INFORMATION:  
APPLICANT: JACOBS, JR., WILLIAM R.  
APPLICANT: BLOOM, BARRY R.  
APPLICANT: COLLINS, DESMOND M.  
APPLICANT: de LISLE, GEOFFREY W.  
APPLICANT: PASCOPELLA, LISA  
APPLICANT: KAWAKAMI, RIKU P.  
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A  
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,255  
FILING DATE: 23-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 25237-20002.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 442 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-255-4

Query Match 4.4%; Score 86.5; DB 1; Length 442;  
Best Local Similarity 23.4%; Pred. No. 0.74; Indels 67; Gaps 12;  
Matches 58; Conservative 34; Mismatches 89;  
OY 55 KYADLGCAAGPNTLLVRIIVOSIDKY-----GOEKNLEPRTIOFLNDLFQNDPNSVF 110  
DB 135 QVAAAGATADP-----VKDYLKQIGKVPPLNABOEVELAKRIENGAFADKLAN-----D 185  
OY 111 KLPSFYRKLE--KENGKRTGSCILISA-----MPGSFYGRLEFPESNHLHSCYSYHW 161  
DB 186 KLAFLKRELEIILAEIDGRRAKNHLLLEANLRLVSLAKRYTGR-----GMLFL----- 232  
OY 162 LSOVPSGLVIELGIG-----ANKGSIVSSKGRPPVQKAYLDOFTKDFTFELR 209

DB 233 -----DLIOGNGILIRAVEKEDYTKGKESTYATWMIROATRAMADOAR---TIRIP 283  
OY 210 ISKELFSR-----GRMLTICICVDEPDPNPDLMDLAINDLIVGLLEEKLDSEFIP 265  
DB 284 VAMVEVINKLARVORQLO-----DLGREPTPEELAKEL--DWTPEKVEVQKXGREIS 336  
OY 266 FTFPSAE 273  
DB 337 LHTPLGED 344

RESULT 13  
US-08-363-255-11  
Sequence 11, Application US/08363255  
Patent No. 5783386  
GENERAL INFORMATION:  
APPLICANT: JACOBS, JR., WILLIAM R.  
APPLICANT: BLOOM, BARRY R.  
APPLICANT: COLLINS, DESMOND M.  
APPLICANT: de LISLE, GEOFFREY W.  
APPLICANT: PASCOPELLA, LISA  
APPLICANT: KAWAKAMI, RIKU P.  
TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A  
TITLE OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,255  
FILING DATE: 23-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 25237-20002.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 442 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-255-11

Query Match 4.4%; Score 86.5; DB 1; Length 442;  
Best Local Similarity 23.4%; Pred. No. 0.74; Indels 67; Gaps 12;  
Matches 58; Conservative 34; Mismatches 89;  
OY 55 KYADLGCAAGPNTLLVRIIVOSIDKY-----GOEKNLEPRTIOFLNDLFQNDPNSVF 110  
DB 135 QVAAAGATADP-----VKDYLKQIGKVPPLNABOEVELAKRIENGAFADKLAN-----D 185  
OY 111 KLPSFYRKLE--KENGKRTGSCILISA-----MPGSFYGRLEFPESNHLHSCYSYHW 161  
DB 186 KLAFLKRELEIILAEIDGRRAKNHLLLEANLRLVSLAKRYTGR-----GMLFL----- 232  
OY 162 LSOVPSGLVIELGIG-----ANKGSIVSSKGRPPVQKAYLDOFTKDFTFELR 209  
DB 233 -----DLIOGNGILIRAVEKEDYTKGKESTYATWMIROATRAMADOAR---TIRIP 283

OY 210 HSKELFSR-----GRMLTCTCKVDEPNPLDLDMAINDLIVEGLLEBKLSDFNIP 265  
 DB 284 VHVAVYINKLARVOROMLO-----DLGREPTPELAKEL--DMTEPKYIEVOKYGEPIIS 336  
 OY 266 FTSPSADE 273  
 DB 337 LHTPLGED 344

RESULT 14  
 US-08-676-444-43  
 ; Sequence 43, Application US/08676444A  
 ; Patent No. 6294325  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wetmur, James G.  
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF THERMOSTABLE  
 ; FILE REFERENCE: MSM95-02  
 ; CURRENT APPLICATION NUMBER: US/08/676,444A  
 ; CURRENT FILING DATE: 1996-07-05  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FASTSEQ for Windows version 4.0  
 ; SEQ ID NO 43  
 ; LENGTH: 649  
 ; TYPE: PRT  
 ; ORGANISM: Streptococcus pneumoniae  
 ; US-08-676-444-43

Query Match 4.4%; Score 86; DB 4; Length 649;  
 Best Local Similarity 20.4%; Pred. No. 1.6;  
 Matches 55; Conservative 44; Mismatches 104; Indels 68; Gaps 10;

OY 144 LPEEEMHFLHSCYVHMLSOVPSGLVIEIGANGSGYSSKGCGRPVOKAYIDOFDND 203  
 DB 393 LPAKETLIDRLTPALVHAERKP-----ANDQDHELDIASIDKAY-DLRE 441  
 OY 204 FTT-----FLIRSKELFSRGRMLTCT-----CKVDEPNPLDLDMAINDL 248  
 DB 442 EASSPELEFFGOMGTLYLFAQSDGXIYIDQAAQERKYTEYIE--SIGNDOSQOL 499  
 OY 249 IVGGLLEBKLSDFNIPFTPSAEVACIYEERGS-----C 284  
 DB 500 LVPIYIEFPADALRLKRMPLLEEVEFLAEYGENOFTLREHPIWMAEELISGIYEMC 559  
 OY 285 EILYL--ETFKAHYDAF-----SIDDDYVRSHEQIKAEVYASLIRSVY-----EP 329  
 DB 560 DMLLTKEYSIKRYAEALAIMSCRSIKANHRIDHSAROLLTOLSCDNPNPCPHGRP 619  
 OY 330 ILASHGEAIMPLDFRLAKAFAKVLHMGK 359  
 DB 620 VLV-HFTKSDMEKMFRIQENHTSLRELK 648

RESULT 15  
 US-08-363-255-5  
 ; Sequence 5, Application US/08363255  
 ; Patent No. 5783386  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JACOBS, Jr., WILLIAM R.  
 ; APPLICANT: BLOOM, BARRY R.  
 ; APPLICANT: COLLINS, DESMOND M.  
 ; APPLICANT: de Lisle, GEOFREY W.  
 ; APPLICANT: PASCOBELLA, LISA  
 ; APPLICANT: KAMAKAMI, RIKU P.  
 ; TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOEISTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto

STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/363,255  
 FILING DATE: 23-DEC-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MONROY, GLADYS H.  
 REGISTRATION NUMBER: 32,430  
 REFERENCE/DOCKET NUMBER: 25237-20002.22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 445 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 ; US-08-363-255-5

Query Match 4.3%; Score 85.5; DB 1; Length 445;  
 Best Local Similarity 23.4%; Pred. No. 0.97;  
 Matches 58; Conservative 34; Mismatches 89; Indels 67; Gaps 12;

OY 55 KVALGCGASGPNLTIVRDIYOSIDKV-----GOEKNELERPTIOIFNDLFONDFNSVF 110  
 DB 138 OVAVAGATADP-----VKDYTLKQIGKVPILNABQEVLEAKRIEAGLFEADKLAN---AD 188  
 OY 111 KLPSFYRKLE--KENGRIKISGLISA-----MPGSFYGRLPRESMHLFHCYCVH 161  
 DB 189 KLAKLRELEITIAEDGRANKHLLLEALRLVYSLAKRYGR-----GMELT----- 235  
 OY 162 LSQVPSGLVIEIG-----ANKSIISSKGCGRPVOKAYIDOFDNDFTFIR 209  
 DB 236 -----DLIOEGMGLIRAVEKFDYTKGKFSYATATWITROAITRAMADOAR---TRIP 286  
 OY 210 HSKELFSR-----GRMLTCTCKVDEPNPLDLDMAINDLIVEGLLEBKLSDFNIP 265  
 DB 287 VHVAVYINKLARVOROMLO-----DLGREPTPELAKEL--DMTEPKYIEVOKYGEPIIS 339  
 OY 266 FTSPSADE 273  
 DB 340 LHTPLGED 347

Search completed: July 27, 2002, 05:40:07  
 JOD time: 3558 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: July 27, 2002, 04:45:09 ; Search time 37.67 Seconds  
(without alignments)  
964.209 Million cell updates/sec

Title: US-09-971-020-1  
Perfect score: 1972  
Sequence: 1 MEQEVLMHNEGEEDSYAK.....KGCYNLTIISLAKPKESDV 378

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614.5	31.2	371	E85430	hypothetical prote
2	577.5	29.3	359	F84513	hypothetical prote
3	533	26.5	323	B86329	hypothetical prote
4	439	22.3	351	A86285	protein F91.6 [lm
5	423.5	21.5	363	E96703	hypothetical prote
6	411.5	20.9	619	T05062	hypothetical prote
7	404.5	20.5	379	T51784	ATPP-like protein
8	401	20.3	348	T51783	ATPP-like protein
9	400	20.3	348	T51781	protein kinase Atpp
10	127.5	6.5	534	C90542	hypothetical prote
11	118	6.0	439	S51378	probable membrane
12	107.5	5.5	999	F72453	probable cytochrom
13	106	5.4	986	T38205	RanBP7/importin-be
14	103.5	5.2	946	G71617	conserved hypotet
15	102.5	5.2	1436	B81704	SRRA antigen/papal
16	102.5	5.2	139742	T39742	hypothetical prote
17	102.5	5.2	2210	RRAKTV	hypothetical prote
18	102	5.2	344	H83928	hypothetical prote
19	101	5.1	405	T12824	hypothetical prote
20	101	5.1	2505	XVRFPA	fatty-acid synthas
21	99.5	5.0	997	T15243	hypothetical prote
22	98	5.0	663	E96705	hypothetical prote
23	98	5.0	2185	GNNYBT	genome polypeptid
24	97.5	4.9	473	F69255	hypothetical prote
25	97	4.9	755	T41912	structural phospho
26	97	4.9	1294	T04278	hypothetical prote
27	97	4.9	1662	T01893	hypothetical prote
28	97	4.9	2185	GNNYSV	genome polypeptid
29	97	4.9	2185	GNNYSH	genome polypeptid

30	96.5	4.9	778	2	A64656	hypothetical prote
31	96.5	4.9	978	2	T00336	hypothetical prote
32	96	4.9	2201	1	GNNYAS	genome polypeptid
33	95.5	4.8	242	2	E97000	lipase-esterase re
34	95.5	4.8	1127	2	S47445	MDM1 protein - yea
35	95	4.8	1407	1	BMYW1	TATA box-binding p
36	95	4.8	2185	1	GNNYB3	genome polypeptid
37	94.5	4.8	401	2	C70159	translation elonga
38	94.5	4.8	865	2	B64618	preprotein translo
39	94.5	4.8	343	2	T42207	breast cancer susc
40	94	4.8	648	2	T41915	hypothetical prote
41	94	4.8	750	2	A56881	prostate-specific
42	93	4.7	1927	2	T25604	hypothetical prote
43	92.5	4.7	260	2	T41554	hypothetical prote
44	92.5	4.7	329	2	T25931	hypothetical prote
45	92.5	4.7	684	2	T32024	hypothetical prote

## ALIGNMENTS

RESULT 1  
E85430  
hypothetical protein At4g36470 (imported) - Arabidopsis thaliana  
C.Species: Arabidopsis thaliana (mouse-ear cross)  
C.Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_Change 16-Feb-2001  
C.Accession: E85430  
R.anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp.  
Nature 402, 769-777, 1999  
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A.Reference number: A85001; MUID: 20083488  
A.Accession: E85430  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-371 <STO>  
A.Cross-references: GB:NC\_001268; NID:97270595; PIDN:CAB80313.1; GSPDB:GN00140  
C.Genetics:  
A.Gene: At4g36470  
A.Map position: 4

Query Match	Best Local Similarity	31.2%	Score 614.5	DB 2	Length 371
Matches 139	Conservative 64	Mismatches 126	Indels 23	Gaps 8	
QY	2	ELQEVLMHNEGEEDSYAKNAS-YNALAKYKPPLEOCIRELIANLPINKCIKIVADLG 60			
DB	5	DMEREFYMTGDKETSYARNSSLOKASDPAKNTLETLOQYKETRP--KSLGIADLG 61			
QY	61	CASGPNLLTVRDIVOSIDKVGQEKNELEPITQIFLNDLFQDNFNSYFALPSFYKRL 120			
DB	62	CSGPNLLSTITPFIKTQVVAHNRPIPIPLPFSIFLNDLPQDNFNFYSFLDPFHEL 121			
QY	121	EKENGRKIGSC--LISAMPGSFYGRLPPEESMFLSCSYVHMLSOVPSGLVIELIGA 177			
DB	122	KRDNNN--GQCPVFIAAYPGSFYGRLEPENTIFHYVASHSLHMTSKVPTALYDOCKSI 179			
QY	178	NKGSIVSKCKRPVQKAYLDQFTKDTTIRIKSKELFRGMLITGCK--VDEPDP 235			
DB	180	NKGVSTCSISSEAVSKAICQFKEDFSIFLCKSKEMVSAGHMYLIIIGREGPDHYDRG 239			
QY	236	NPL--DILDNAINDLIVEGLLEEKLDSEFNIPFTPSAEVKCYIEEBOECILYLETFK 293			
DB	240	NSFWELLSISINDLVAQGETEEELKLDSDYDMFAPADEIRGEVDKSGSEFLRMLME 299			
QY	294	AHYDAASISD-DYPRSHQDKAEVVASLIRSYEPIILASHGCAINPDPF 344			
DB	300	VKKDKGNTGEDISY-----GRAVAKTVBAVQESMLVQHGEKILDKLF 342			
RESULT 2					
F84513					
hypothetical protein At2g14060 (imported) - Arabidopsis thaliana					

C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: F84513  
 R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Crokin, I.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;  
 Nuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402: 761-766, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana  
 A:Reference number: A84420; MUID:20083487  
 A:Accession: F84513  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-359 <STO>  
 A:Cross-references: GB:AE002093; NID:94388826; PIDN:AD19781.1; GSPDB:GN00139  
 A:Gene: At2g14060  
 A:Map position: 2

Query Match 29.3%; Score 577.5; DB 2; Length 359;  
 Best Local Similarity 37.6%; Pred. No. 1,2e-36;  
 Matches 142; Conservative 72; Mismatches 131; Indels 33; Gaps 12;

9 MNGEGDTSTAAKASYNAL-AKYPELEOCIRELLRANLPINNCIVVADIGASGPT 67  
 1 MKGSTDHSTAINSHKORSVFEIOLPVTINVRMLAK--GFPCIVADIGCSIGNT 58  
 68 LTVRIQVOST-DKVGQEKNELEPRTIQIFLNDLFONDNSVFKLPSPYRKLEKENG 126  
 59 VLMAKSLATITESTYQAKSKNP---PEIDYLDLNDENFTFTFLFHSFQEKLRPE-- 112  
 127 KIGSCLISMPSEYGRPLPESNMHLASGYVHMLSOVSLVEIGLIGANKSIIYSK 186  
 113 VKRMVSVSPSEYGRPLPESNMHLASGYVHMLSOVSLVEIGLIGANKSIIYSK 166  
 187 GCRPVQAKYLDQFTKPTTFLRIHSEKLPKRGMLTICI-CKVDEF---DEPNPDL 242  
 167 PYSNVYKSYLQFKIDSLFLKMRSEVYVNGHMLFTVGRKYSDDLTKSCDFQWVSL 226  
 243 MAINDIVGLLEEKLDSEFNIPFTPSAEVAKCIYEBSGCELIYETFAKHAIDAFSI 302  
 227 DCLDLASGPFNDMSKSPFNNPNEEVEVREFLKGSFEIKIRK--DHVYVKI 284  
 303 -----DDDDPVSHQIKAEVVAALIRSVPEPIASHPEEALIMPLFLAKHAAYLHM 357  
 285 DREDEDEQSILDEAGIKH--ASMARCTEPPLVAHGEDALIEVFNKHYVAKYLSV 341  
 358 GKGCYNN---LITSLAK 372  
 342 SNRRKMTLVIVSLTRK 359

RESULT 3  
 866329  
 A:Title: Hypothetical protein F14P1.3 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
 C:Accession: B86329  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
 ansen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408: 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maitl, R.; Marzella,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: B86329  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-323 <STO>  
 A:Map position: 1

A:Cross-references: GB:AE005172; NID:97955588; PIDN:AAF8406.1; GSPDB:GN00141  
 A:Gene: At2g14060  
 A:Map position: 1

Query Match 26.5%; Score 523; DB 2; Length 323;  
 Best Local Similarity 31.1%; Pred. No. 1.6e-32;  
 Matches 122; Conservative 77; Mismatches 101; Indels 92; Gaps 10;

1 MELOEVLHNGEGDTSTAAKASYNALAKV-KPELEOCIRELLRANLPINNCIKKIVADL 59  
 1 MEVNVLMHMKNGESTYAKNSTAOSNITISLGRVMDALTKIMSN--SEISISIGIDL 58  
 60 GCASGPTLLTVRIQVOSTDKVGQEKNELEPRT--IQIFLNDLFONDNSVFKLPSEFY 117  
 59 GCSSGPNLSLISNIVDTIHLNCP---DLDRPVLELVSILNDLPENDNYICASLPREY 114  
 118 RLKRENGRKIG-----SCLISAMPGSFYGRPLPESNMHLASGYVHMLSOVSG 168  
 115 ---DRVNNKNEGIGFGRGEGECFSAVPSFGYGRPLPESNMHLASGYVHMLSOVSG 171  
 169 L-----VIEIGIGANKSIIYSKSGCRPVQAKYLDQFTKPTTFLRIHSEKLPKRGML 223  
 172 SNRRKMTLVIVSLTRK 359

224 TCICVDFEPEPNLDMALINDIVGLLEEKLDSEFNIPFTPSAEVAKCIYEBSG 283  
 196 -----DDDDPVSHQIKAEVVAALIRSVPEPIASHPEEALIMPLFLAKHAAYLHM 357  
 284 CEILYETFAKHAIDAFSIIDDDY--VSHQIKAEVVAALIRSVPEPIASHPEEALIMPLFLAKHAAYLHM 357  
 230 FSIKRLSEPLIDEGSISEESYDVIKREALASGRVSNTRIVAVEPMLEPFGENV 289  
 340 MEPLFHLAKHAAYLHMKGCCYNNLITSLAK 372  
 290 MDELFEKAKYVGEYFVSPPRAYIVLTLVR 321

RESULT 4  
 A86285  
 A:Title: Protein F9L1.6 [Imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: A86285  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
 ansen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408: 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maitl, R.; Marzella,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: A86285  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-351 <STO>  
 A:Cross-references: GB:AE005172; NID:95103811; PIDN:AA039641.1; GSPDB:GN00141  
 A:Gene: F9L1.6  
 A:Map position: 1

Query Match 22.3%; Score 439; DB 2; Length 351;  
 Best Local Similarity 30.8%; Pred. No. 4.8e-26;  
 Matches 111; Conservative 63; Mismatches 140; Indels 46; Gaps 9;

9 MNGEGDTSTAAKASYNALAKV-KPELEOCIRELLRANLPINNCIKKIVADIGASGPT 67  
 1 MKGSTDHSTAINSHKORSVFEIOLPVTINVRMLAK--GFPCIVADIGCSIGNT 58



A:Molecule type: DNA  
 A:Residues: 1-379 <DEL>  
 A:Cross-references: EMBL:AL391254  
 A:Experimental source: cultivar Columbia; BAC clone F28D10  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 23/3; 235/3  
 A:Note: F28D10\_60

Query Match 20.5%; Score 404.5; DB 2; Length 379;  
 Best Local Similarity 28.5%; Pred. No. 2.3e-23;  
 Matches 109; Conservative 77; Mismatches 138; Indels 59; Gaps 13;

QY 12 GGGTSTAKNASTNLAAYKFFLEDCIRELL--RANLPINIKCIKIVADLCAGSPVTL 69  
 DB 10 GGGNSTRDRSKTQGLVLA--AKEKINEISTKLDIDFTSLVNIADFCSSGPTFT 66  
 QY 70 TVRDIVOSIDKVGQEKNELEPRTQIFLNDLFONDNSVFKLLP--SFYRKLEKNGR 127  
 DB 67 AVQTLIDAVENKKYKKS--IE--FOVFNDSSNNDENTLFTLPPARLY----- 112  
 QY 128 IGSGLISAMPGSFYGRLPPEESMHFLHSCYSVHLSQVPSGVVIELGIGANKGSIVSSK 187  
 DB 113 ---FAGGVGSGFGRVLPRLNSLHGVSAYSLHRTSKPEYVDRDSDPVWNR-DIHCS-G 166  
 QY 188 CRPPVOKAYIDQFTKDTFTFLRIHSEKELFSRGLMLTLCCK--VDEPD--EPNPLDLD 242  
 DB 167 SSKREKATLYGQKIDVGSFLNARQELVSGLLLLGSCRPNQVMEFEGMMIDFIG 226  
 QY 243 MAINDLIVGLLEEKLDSEFNIPFTPSAEVVKCIYEESCEILYLETFNAHYDAFSL 302  
 DB 227 ASLMEINAGLIDQGLDQKLPFIAPADDELKQIIDNCTIEVFENT--IHAKGEYPL 285  
 QY 303 DDOXPRVSHQIKAEVYASLRSVPEPLASHRGEALMPDLFRLAKRAKAYLA----- 356  
 DB 286 DPEFLTVSFKYTVGGSVASL-----FGQDGEKTEFLVAKETOELPQIAKAK 333  
 QY 357 -----MGKCYNNLTISLAK 371  
 DB 334 PGMOYLIVLRNCFHDLFRSLKR 356

RESULT 8  
 T51783  
 AtPP-like protein - Arabidopsis thaliana  
 N:Alternate names: protein F28D10\_50  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C:Accession: T51783  
 R:Delaney, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Rudd, S.; Le  
 submitted to the Protein Sequence Database, August 2000  
 A:Reference number: Z25454  
 A:Accession: T51783  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-348 <DEL>  
 A:Cross-references: EMBL:AL391254  
 A:Experimental source: cultivar Columbia; BAC clone F28D10  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 23/3; 238/3  
 A:Note: F28D10\_50

Query Match 20.3%; Score 401; DB 2; Length 348;  
 Best Local Similarity 29.6%; Pred. No. 3.8e-23;  
 Matches 106; Conservative 76; Mismatches 124; Indels 52; Gaps 13;

QY 67 TLTVRDIVOSIDKVGQEKNELEPRTQIFLNDLFONDNSVFKLLP--SFYRKLEKEN 124  
 DB 64 TETAVQTLIDAVENKKYKKS--IEGIEFQVFNDSSNNDENTLFTLPPARLY----- 115  
 QY 125 GRIKISGLISAMPGSFYGRLPPEESMHFLHSCYSVHLSQVPSGVVIELGIGANKGSIVS 184  
 DB 116 ---FAGGVGSGFGRVLPRLNSLHGVSAYSLHRTSKPEYVDRDSDPVWNR-DIH 167  
 QY 185 SSGCRPPVOKAYIDQFTKDTFTFLRIHSEKELFSRGLMLTLCCK--VDEPD--EPNPLD 239  
 DB 168 S-GSKREKATLYGQKIDVGSFLNARQELVSGLLLLGSCRPNQVMEFEGMMID 226  
 QY 240 LIDMAINDLIVGLLEEKLDSEFNIPFTPSAEVVKCIYEESCEILYLETFK--AHYD 297  
 DB 227 FIGSLMEINAGLIDQGLDQKLPFIAPADDELKQIIDN--KCFTEKPEKISHAK 283  
 QY 298 AAFSIDDYPRVSHQIKAEVYASLRSVPEPLASHRGEALMPDLFRLAKRAKAYL 355  
 DB 284 GEYPLD-----PEYLTSAFKYTVGGSVASLFGQDGEKTEFLVAKETOELM 329

RESULT 9  
 T51781  
 protein kinase AtPP-like protein - Arabidopsis thaliana  
 N:Alternate names: protein F28D10\_30  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C:Accession: T51781  
 R:Delaney, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Rudd, S.;  
 submitted to the Protein Sequence Database, August 2000  
 A:Reference number: Z25454  
 A:Accession: T51781  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-348 <DEL>  
 A:Cross-references: EMBL:AL391254  
 A:Experimental source: cultivar Columbia; BAC clone F28D10  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 23/3; 238/3  
 A:Note: F28D10\_30

Query Match 20.3%; Score 400; DB 2; Length 348;  
 Best Local Similarity 30.8%; Pred. No. 4.6e-23;  
 Matches 106; Conservative 66; Mismatches 126; Indels 46; Gaps 12;

QY 12 GGGTSTAKNASTNLAAYKFFLEDCIRELL--RANLPINIKCIKIVADLCAGSPN 66  
 DB 10 GGGNSTRDRSKTQGLVLA--AKEKINEISTKLDIDFTSLVNIADFCSSGPTFT 63  
 QY 67 TLTVRDIVOSIDKVGQEKNELEPRTQIFLNDLFONDNSVFKLLPSEFYRKLEKENR 126  
 DB 64 TETAVQTLIDAVENKKYKKS--IEGIEFQVFNDSSNNDENTLFTLPPARLY----- 113  
 QY 127 KISGLISAMPGSFYGRLPPEESMHFLHSCYSVHLSQVPSGVVIELGIGANKGSIVSSK 186  
 DB 114 K--FAGGVGSGFGRVLPRLNSLHGVSAYSLHRTSKPEYVDRDSDPVWNR-DIH 168  
 QY 187 SSGCRPPVOKAYIDQFTKDTFTFLRIHSEKELFSRGLMLTLCCK--VDEPD--EPNPLD 241  
 DB 169 GSKREKATLYGQKIDVGSFLNARQELVSGLLLLGSCRPNQVMEFEGMMID 228  
 QY 242 LIDMAINDLIVGLLEEKLDSEFNIPFTPSAEVVKCIYEESCEILYLETFK--AHYD 300  
 DB 228 GSSLDLAKGLIDQGLDQKLPFIAPADDELKQIIDN--KCFTEKPEKISHAK 280  
 QY 301 SIDDYPRVSHQIKAEVYASLRSVPEPLASHRGEALMPDLF 344  
 DB 281 QENEPD-----LDPEFLTVSFKYTVGGSVASLFGQDGEKTEFLVAKETOELM 318

Query Match	6.5%;	Score 127.5;	DB 2;	Length 534;
Best Local Similarity	21.4%;	Pred. No. 0.056;		
Matches 71;	Conservative 47;	Mismatches 107;	Indels 107;	Gaps 16

RESULT 11

probable membrane protein YLR360w - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: hypothetical protein L8039.11  
C:Species: *Saccharomyces cerevisiae*  
C:Date: 23-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 04-Mar-2000  
R:Du, 2.  
submitted to the EMBL Data Library, December 1994  
A:Description: The sequence of S. cerevisiae cosmid 8039.  
A:Reference number: S51377  
A:Accession: S51378  
A:Molecule type: DNA  
A:Residues: 1-439 <DD2>  
A:Cross-references: EMBL:U019103; NID:9609404; PID:9609445; MIPS:YLR360W  
C:Genetics:  
A:Gene: SGD:VPS38  
A:Cross-references: SGD:S0004352; MIPS:YLR360w  
A:Map position: 1R  
C:Superfamily: *Saccharomyces cerevisiae* probable membrane protein YLR360w  
C:Keywords: transmembrane protein  
E:83-99/Domain: transmembrane #status predicted <TM>

RESULT : 12

C:Probable cytochrome C-type biogenesis protein APE2274 - Aeropyrum pernix (strain K1)  
 C:Species: Aeropyrum pernix  
 C>Date: 20-Aug-1999 #sequence=revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C:Accession: F72453  
 R:Ravaraibayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatahara, Y.; Jin-no, K.; Tawa, H.; Takamizawa, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.  
 DNA Res. 6, 83-101, 1999  
 A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenearchaeon, Aero  
 A:Reference number: A72450; MUID:99310339  
 A:Accession: F72453  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-999 <RKM>  
 A:Cross-references: DDBJ:AF000064; NID:95105945; PIDD:BA81266.1; PID:d1045072; PID:g  
 A:Experimental source: strain K1  
 C:Genetics:  
 A:Gene: APE2274

```

Query Match 5.58% Score 107.5: DB 2: Length 999;
Best Local Similarity 20.0% Pred No 4.3;
Matches 84: Conservative 71; Mismatches 157; Indels 107; Gaps 20;

QY 4 QEVLMANGEDBDTSYAKNMSYNILAKYKFLBECIFELLRANLPIN-KGIKADIGCA 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 565 KRLNMWDEDSITIRE---YRLASNEQS---DRTIOTLLKASANSERGVFTSHGVA 619
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 SGPNLLIVPIYOSIDKGOEKNELRPITOFILFLDQNFQDNFVSRYKLLSPRYRLEK 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 620 DAAVVDVATGGININIOITAG-ENVLLEDPLFLEVTIDP-----KLDP 660
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 ENGRKIGISCLLSAMPGSFYGRLLFPRESNHF-----LHSCSYVHMLSGVPSGLVTEL 173
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 661 EICRIEGALSLV-----FYPRRLVYVIGISPSVLDPIYSYLVPRPREVEINL-DDI 711
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 GIGAKGKISYSKRCRPVQKAVLDQFKDPTFLRIHNSKEL-----FSKGRM 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 712 TVNMEVVYVSTG--SSIEGVVSGQSVLFEQVAILRVVSGEELSFSGMNIELPYQLDGRGE 769
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 LITGICK--VEFPEPRLPDLIDMAINIL---VEGLLEEKIKDSINILPPTTPAAEEKVC 776
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```



Db 770 FYPMVKGQAEVLD-----DLSSISDLESGIAGLAGEMDNFVPRRACVSLFL 824  
 Qy 277 IVEEESCCILILEFKAHYA-----AFSIDDYPRSHEDIKAEVYASLRSVPEPIIA 332  
 Db 825 FMEYNEPEVADLR-FEANGEAIGHGLVID-----TILRGLTNYITVQAPLVS 875  
 Qy 333 SHEGEAIMDLEFRLAKH-----AAKVLHGKGCYNNLLISLAKPER 375  
 Db 876 GHGGE-----YHELMVYVLLNEAMNLRPEEYLALASVMAAG-----YN--IASIVSSPSK 923

RESULT 13  
 T38205  
 RanpP7/Importin-beta/Cseip homolog - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
 C:Accession: T38205  
 R:Gishchuk, K.; McIntosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream, M.  
 Submitted to the EMBL Data Library, February 1996  
 A:Reference number: 221778  
 A:Accession: T38205  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-986 <DEV>  
 A:Cross-references: EMBL:Z69730; PIDN:CAA93604.1; GSPDB:GN00066; SPDB:SPAC22H10.03c  
 A:Experimental source: strain 972H-; cosmid c22H10  
 C:Genetics:  
 A:Gene: SPDB:SPAC22H10.03c  
 A:Map position: 1  
 A:Introns: 36/1; 776/3; 833/2; 873/1; 930/1; 947/3

Query Match 5.4%; Score 106; DB 2; Length 986;  
 Best Local Similarity 19.6%; Pred. No. 5.5; Mismatches 130; Indels 148; Gaps 19;  
 Matches 83; Conservative 62;

Db 529 SVGKVPILSLQPMLEVL-----SQYAKSSDEALVLLVEAIISSAVLDDA 575  
 Qy 27 ALAKVRF--LEQCIRELLRANLPNINKCIKVAADGASGPNLLTVNDIVQSIDKVG 84  
 Db 529 SVGKVPILSLQPMLEVL-----SQYAKSSDEALVLLVEAIISSAVLDDA 575  
 Qy 85 EKNELEPPTIOIFLN-----DLFQ-----NDFSVFKL-LPSFYRKL 121  
 Db 576 KAMELENSVPIPLFVLVATNADPYIGLIEPTFEDIIHANNNESMCITLPELLOVN 635  
 Qy 122 KEN-----GRIGSCIL-----SAMPGSFYGRLPPEESMHFLHSCYSVHMLSQVPSG-- 168  
 Db 636 QEDPIVWNGATILSLCLIRAGPSPLPNGFYGLP-----FYKIITIHSGDTE 684  
 Qy 169 -----LVIELGIGANKGSIYSSKGRPPVQAKAYIDQFTKPTTF-- 207  
 Db 685 LIDLSGELIKGLLEKPTQLELETERISGSGSFQITLF-----TLHQLDKESDSDACFIVG 739  
 Qy 208 -----LRHSKELSRGMILITCICVDEDEPNPLDLDMAINDLIVEGLLEEKLDSE 262  
 Db 740 PILLELADHASQMDVLDISLSCIKRLAIAEQPRFQSIIVFAKLIVK-----DGL 791  
 Qy 263 NIFFTPSAEEYKCIIVEEG--SCETL-----YLETER-----AHYDAFISIDD 305  
 Db 792 GMMHFTLSS-----LLMGOGLTAFVLYMTCNDNFVYSNKNKSIICIMTKIYFSDS- 845  
 Qy 306 YPRSHEDIKAEVYASLIR-----SYEPIILASHGEAIMDLEFRLA 348  
 Db 846 -PLDSDVQVKGELISHSRKRTITSQSKLHPEYSVSVGEKIL-----RLDSEEVSL 898  
 Qy 349 KHA 351  
 Db 899 KDA 901

RESULT 14  
 G71617  
 Seta antigen/papain-like proteinase with active Cys PEB0330c - malaria parasite (Plasmodium falciparum)  
 C:Species: Plasmodium falciparum

C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
 C:Accession: G71617  
 R:Gardner, M.C.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pereira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.  
 Science 282, 1126-1132, 1998  
 A>Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
 A:Reference number: A71600; MUID:99021743  
 A:Accession: G71617  
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-946 <GAR>  
 A:Cross-references: GB:AE001387; GB:AE001362; NID:g3845152; PIDN:AAC71855.1; PID:g384  
 A:Experimental source: clone 307  
 C:Genetics:  
 A:Gene: PEB0330c  
 C:Superfamily: Plasmodium vivax setline-repeat antigen

Query Match 5.2%; Score 103.5; DB 2; Length 946;  
 Best Local Similarity 20.6%; Pred. No. 8.1; Mismatches 102; Indels 137; Gaps 18;  
 Matches 76; Conservative 54;

Db 20 KNASYNLATAKVPLEQCI-----RELLRANLPNINKCIKVAADGASGPNLLTV 71  
 Qy 284 ENCYHCTLAKKVDNSNCEFNVYKAEKELINKKKEKTEKGEDEDLSEOKLEESI 343  
 Db 72 RDIYOSIDKVGQERK-----NELEPPTIOIFLNLPQNDENSVFYKLLPSFYRKL 121  
 Qy 344 DNLISNTYKIKYESKDKERKSHNNKKELVTE-----ELNSVLKTELLNTYCKL 394  
 Db 122 KENR-----KIS-----CLISAMPGSFYGRLPPEESMHFLHSCYSVHMLSQVPSG-- 158  
 Qy 395 KEVDKSGMDHREIDEDIRNMLIRLKAHPG-----ESTVINEKLRNLPALCFK 445  
 Db 159 -VHMSQVPSGLVTELGIGANKGSIYSSKGRPPVQAKAY--LDQFTKPTTFELRHS 212  
 Qy 446 NIEWLVN-----KGLLSNKKIONLSTNYNTDLESEYDEYEFIS-- 489  
 Db 213 KEFLSRMLTICGVDEDEPNPLDLDMAINDLIVEGLLEEKLDSEFNIPFTPS-- 270  
 Qy 490 -----DDMEFKMNGVIDLSLF-----NEKKLS--PYFRNKY 522  
 Db 271 -----AEYKCI-----VEEGSCETLILETFKAYDAFASISDDYPR-- 312  
 Qy 523 CNNEYCDKKDKTGICISKIEVEEGNGGLCMIRASKLHET-----TRCKRGIGH 573  
 Db 313 QIRAEVYAS 321  
 Qy 574 RSSALIVAN 582

RESULT 15  
 B81704  
 conserved hypothetical protein TC0424 [imported] - Chlamydia muridarum (strain N199)  
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MOpn  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000  
 C:Accession: B81704  
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke  
 C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe  
 Nucleic Acids Res. 28, 1397-1406, 2000  
 A>Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39  
 A:Reference number: AB1500; MUID:20150255  
 A:Accession: B81704  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1436 <TET>  
 A:Cross-references: GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF39280.1; PID:g719  
 A:Experimental source: strain N199 (MOpn)  
 C:Genetics:  
 A:Gene: TC0424

Query Match 5.2%; Score 103.5; DB 2; Length 1436;

Best local similarity 18.64; Pred. No. 14; \*  
Matches 74; Conservative 79; Mismatches 145; Indels 99; Gaps 17;

```
OY 2 ELDEEVH-WNEBEGTSTAKKASYNLALAVKFLFEOCIREFLRANLPINKCIKYNADLG 60
Db 381 EIEDAHHEICIEDGISPYIDP-----OVRIYTKCLREELKDLGKTDEELKPDLS 432
OY 61 CASGPTLLTVRDIVOSID-KVGOEKN--ELERPTIQIFLNDLFO--NDENSVFKLP 114
Db 433 KIQ-RSVCLFATSVVSLLEGVMGVSEKSIKEIETVRELGSTLLQGLSGGITPLD 491
OY 115 SFYRKLEKENGKRIKISCLISAMPGSFYGRLEFPRESMHFLHS-----CYSV 159
Db 492 NVKKAIRQ--GRALSNELROSI-----QIAPERFRHRLQAKVEKLOGFIRDPKMGASAV 543
OY 160 HMLSOVP-----SGVIEELGIGANKSIIYSSKGRPPVOKAYLDQFTKDFTFPL 208
Db 544 HLSQETLEOKRQLDLKLTGIGITLSDMETRYSVK---ETKLFHYMEDFEKETEKFL 599
OY 209 RIHS-----KELFSRGRMLTLCICKYDEDEPNPLDLMAINDLIVEGLLE 256
Db 600 NSHSAVAESCSLDCSVEELKDCDALNADLNIEKVMNPADYESAREFKQLISDLAQV 659
OY 257 EKLDSENIPEFTPSAEVKCIYEEEGSCILLIETFAHYDA-----AFST- 302
Db 660 EQLDQUSVP-----ICERVSGRKLLNTLSHPTLQKKELEKRAALEAFTSG 708
OY 303 -DDDYPRSHQIKA---EYVASLIRSV--YEPIL 331
Db 709 EDPEFPVRKEETLDVWSSGYDYLSNLLGKINSFESIL 745
```

Search completed: July 27, 2002, 05:41:00  
Job time: 331 sec



```

OY 208 -----LRHSKELFRSGMILLTICIKYDEDEPNLDDAINDLYEGLEEEKIDSF 262
DB 740 PILLELADIASOMVLOSILSCIKRALAEOPRFQISITIVFAKLYK-----DSL 791
OY 263 NIFFTPSAEYKCIYEEBEG--SCETL-----YLETET-----ANYDAFSTDD 305
DB 792 GMMHFTSS-----LLNEOGLTAEVMTWCDNFYSENFENSIICIMTKTSPDS- 845
OY 306 YPVRSHEQIAEYVASLIR-----SYVEPIASHGFEAIMPDLEFRLA 348
DB 846 -PLDSDYQVKGELISHSRNITRSQSKLHPEXSVSVGEKIL-----RLLSPEFVSLS 898
OY 349 KHA 351
DB 899 KDA 901

RESULT 2
ID PROTO_TACY STANDARD: PRT: 2210 AA.
AC P20430/
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE RNA polymerase (EC 2.7.7.48).
GN
OS Taccaribe virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11631;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89243206; PubMed=2718387;
RA Iapalucci S., Lopez R., Rey O., Lopez N., Frazer-Fernandez M.T.,
RA Cohen G.N., Lucero M., Ochao A., Zakin M.M.
RT "Taccaribe virus L gene encodes a protein of 2210 amino acid
RT residues".
RL virology 170:40-47(1989).
CC -I CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC The European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J04340; AAA47901.1;
DR PIR: A31468; RRPXTV.
RW RNA-directed RNA polymerase: Transferrase.
SQ SEQUENCE 2210 AA; 252230 MW; EACF01C32761024F CRC64;

Query Match 5.28; Score 102.5; DB 1; Length 2210;
Best Local Similarity 21.58; Pident. No. 6.5; Index 145; Gaps 23;
Matches 89; Conservative 59; Mismatches 121;

OY 34 FLEOCIRELLR-----ANLPNICKIVADLGCASGPTLLTVYDIVQSIDRV 81
DB 413 WVNCSKILIRSQOQIWSQISVMRYRDLKLSIA-----QTSSDPIPIRY--SA 462
OY 82 GOEKNELERPTIQFLNDLFONDENSVEFKLPSFRKLKENGKRGKISGASAMPGEV 141
DB 463 GGNFNECKHKTFPHM-MSDAEOVE--AFKILSS-----VSLSIINSMTSFS 506
OY 142 GRLE---PRESHF---LHSCVSVHLSGVPEGLV-----ELIG 175
DB 507 SRLINKEKSYKFGNVARLRCGYOGRF--LTGGLVILFYKTKGERSGCKSYTCEDGV 564
OY 176 GAKGSIYSKCKRPPVOKAALDOFTK-----DFTFLIRHNSKELFSNGM 221
DB 565 LYKGSFY-----CDP--KRFPLIFSOEVLVEKMDMTWLDPSDLKAVISKELR--LL 616

```

```

OY 222 LITGICVDEDEP-----NPDLDD-----MAINDIYEGL----- 253
DB 617 LLSLTCAPSRRNOVFLQGRFLMAYSNQFHHVDSLKLEKVECMSSSEVYVORLAVDLFQ 676
OY 254 -LEEEKIDSPNIFFTPSAEYKCIYEEBEGSCETLLEYETFKAHYDAFSTDDYVPVRSHE 312
DB 677 CLLEGVDS--DVEF---ARRKYLANSYLCILITKET-----PDLRLTD 716
OY 313 QIKR--EYVASLIR-----SYVEPIASHGFEAIMPDLEFRLAKHAQVLMGKC 361
DB 717 QIKCFEFTIEPKIDFCNIVPNSLNGLTFEAOEGMMDGLDKFYSKTL---KDC 767

RESULT 3
ID PAS_RAT STANDARD: PRT: 2505 AA.
AC P12785; 064717; 009167; 009190;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1999 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Fatty acid synthase (EC 2.3.1.85) [includes: EC 2.3.1.38; EC 2.3.1.39;
DE EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14].
GN FASN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89240686; PubMed=2717611;
RA Amy C.M., Witkowski A., Nagert J., Williams B., Randhawa Z.,
RA Smith S.;
RT "Molecular cloning and sequencing of cDNAs encoding the entire rat
RT fatty acid synthase".
RL Proc. Natl. Acad. Sci. U.S.A. 86:3114-3118(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RA Beck R.F., Schreggmann R., Stathopoulos I., Klein H., Hoch J.,
RA Schweitzer M.;
RT "The fatty acid synthase (FAS) gene and its promoter in Rattus
RT norvegicus".
RL DNA Seq. 2:359-386(1992).
RN [3]
RP SEQUENCE OF 75-2505 FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Mammary gland;
RA MEDLINE=89128431; PubMed=2915923;
RA Schweizer M., Takabayashi K., Beck R.F., Schreggmann R.;
RT "Rat mammary gland fatty acid synthase: localization of the
RT constituent domains and two functional polyadenylation/termination
RT signals in the cDNA".
RL Nucleic Acids Res. 17:567-586(1989).
RN [4]
RP SEQUENCE OF 2085-2505 FROM N.A.
RX TISSUE=Mammary gland;
RA MEDLINE=88087240; PubMed=2891707;
RA Nagert J., Witkowski A., Mikkelson J., Smith S.;
RT "Molecular cloning and sequencing of a cDNA encoding the thioesterase
RT domain of the rat fatty acid synthase".
RL J. Biol. Chem. 263:1146-1150(1988).
RN [5]
RP SEQUENCE OF 1921-2324 FROM N.A.
RX TISSUE=Mammary gland;
RA MEDLINE=87246646; PubMed=3109907;
RA Witkowski A., Nagert J., Mikkelson J., Smith S.;
RT "Molecular cloning and sequencing of a cDNA encoding the acyl carrier
RT protein and its flanking domains in the mammalian fatty acid
RT synthetase".
RL Eur. J. Biochem. 165:601-606(1987).
CC -I- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.

```

Query Match  
Best Local Similarity 21.4% Score 101; DB 1; Length 2505;  
Matches 96; Conservative 54; Mismatches 132; Indels 166; Gaps 22.

FT CONFLICT 2085 2085 C -> P (IN REF. 4).  
FT CONFLICT 2106 2106 A -> V (IN REF. 1 AND 5).  
FT CONFLICT 2296 2296 Y -> H (IN REF. 1 AND 5).  
SO SEQUENCE 2505 AA; 272647 MW; 5810EC13D37F3114 CRC64;

QY 52 KCIKADGACG-----GPNLLTV--RDYSDIXV-----OEKNLEPRT 94  
DB 1463 KCLLSNLSTSHYPRKLPDSESLQKLESDLVNMYVNDGAMCARHQLDQDPSEQTA 1522  
QY 95 QIFLNDLFONDENV-----FLLESFYRIKLENGRKT---GSCLI 133  
DB 1523 HAFVNVLTGRGLASIRWVSSPLKHKMOPSSGALQCLTVYASL--NFRDMLATGSLP 1579  
QY 134 SAMPG-----SEYGR-----LPEPSNHLFSCSYVHMLSOVPSGLVIEL 173  
DB 1580 DAIPKMASRDCMLGMFEFSGRDKCGRRYMGVLVPAEGL-ATVLLSLDLELMPVPSMTLEE 1638  
QY 174 -----GIGANKSGIYSSKGR-----PPVQ 193  
DB 1639 AASVYVYTTATYASLYVYGRIOGHETVILHSGSGVQQAIAISLSCRFETTVGSAEK 1698  
QY 194 KAYLD-OETK-DEFTFLIRHSKELEFSRGMRLTICICVDFEDPDPNLDLMAINDIIVE 251  
DB 1699 RAYLDARPPOLDTDSF--ANSRDTSPEDQVHLTHHGKGG-----VLDVINS--- 1741  
QY 252 GLEEEKLSDSNIEFFFPASAEKQICVDEBSCEI-----LYLETFRAH-- 295  
DB 1742 --LAEEKQA-----SYRCLAQHGREFLEIKGFSDLSNNHPLGMAIFLKAVTFHGI 1788  
QY 296 -YDAFSTIDDDYPYRSHEDQKAEVYASLRVYEPILASHEGATIMPLDLEHRLA--KHAA 352  
DB 1789 LLDALFEBAND---SKREVALKLAGIRDGVKPFILCYTFPRAQYEDAFRMAQGHIG 1844  
QY 353 KYL-----HNGKGCYNNLIISLAK 371  
DB 1845 KYLVQVREPEBPAALPEAOPTLISLAK 1872

RESULT 4  
BP28\_HUMAN  
ID BP28\_HUMAN STANDARD; PRT. 2144 AA.  
AC Q9H583; G9NMW23;  
DT 16-OCT-2001 (Rel. 40, Created).  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Protein BAP28.  
GN BAP28.  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OC NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A. AND VARIANTS S-1694; A-1854; D-1967 AND 6, 2017.  
RA Bougueret L., Chumakov I., Barry C., Cohen-Akenline A.,  
RT A novel BAP28 gene and protein.  
RT Patient number W00100669, 04-JAN-2001.  
RN [2]  
RP SEQUENCE OF 1534-2144 FROM N.A.  
RA Cobley V.  
RN Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1777-2144 FROM N.A.  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,  
RA Wagaatsuma M., Hosokiri T., Raku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono T., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuo T.,

RA Ntomo'ya K., Iwayanagi T.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE BAP28 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 HEAT REPEAT.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: AX067150; CAC36776.1;  
 DR EMBL: AL336105; CAC35948.1; ALT\_INIT.  
 DR EMBL: AK001223; BAA31564.1; ALT\_INIT.  
 DR INTERPRO: IPR000357; HEAT\_REPEAT.  
 DR PROSITE: PS50077; HEAT\_REPEAT; FALSE\_NEG.  
 KM Polymorphism.  
 FT REPEAT 2106 2142 HEAT.  
 FT VARIANT 1694 1694 N->S.  
 FT VARIANT 1694 1694 /FTID-VAR\_010939.  
 FT VARIANT 1854 1854 V->A.  
 FT VARIANT 1854 1854 /FTID-VAR\_010940.  
 FT VARIANT 1967 1967 N->D.  
 FT VARIANT 2017 2017 /FTID-VAR\_010941.  
 FT VARIANT 2017 2017 E->G.  
 FT SEQUENCE 2144 AA; 24235 MW; D66816E7B8C9B7 CRC64;  
 SQ  
 Query Match 5.1%; Score 100.5; DB 1; Length 2144;  
 Best Local Similarity 19.4%; Pred No 9;  
 Matches 98; Conservative 79; Mismatches 160; Indels 167; Gaps 28;  
 Oy 9 MNEBEGTSTAKRASY-NMLAKYKPL--EQCIKRELRANLENKICKVA-----57  
 Db 609 INDDTESAKMKATILSKSGCSGCHPLKMEALLENVICKTKP--GKLIGVANKQMI 666  
 Oy 58 -----DLGASGPTLTVNDIVQISIDKYGQEK-NELERTIOIFL-----NDLQ 103  
 Db 667 LLDNINMG--DPSSML--KMWEDISVGEESFNLMOKYTFVILSVLSCSSLKE 720  
 Oy 104 NDFN--SVFKLLPSEFKLEKENGKRGISCLISA--MPGSFYGLPPEBSM-----HF 152  
 Db 721 THPEFAIRVESLLOKKIKKLES-----VITAVEISEWHIELMDRGIPVELWAHY 771  
 Oy 153 LASCYSVHMLSQVPS-GLVIEIGANGKSGISYSGKCRP-----PYOKAYLDOFTK 202  
 Db 772 VEELNSTGQRAVVDSEFLVPSL--KRTIYALKAPKFPFGDITWNPBQ--LKEDSR 823  
 Oy 203 DE-----TFPIRISKLEPFRGMILLTICIKV-----DEED 233  
 Db 824 DYHLHLIGLFEMMLGADAVHFRVLMKLFKVLHEDVFO-----LFKFCVLMYGGSSLS 878  
 Oy 234 EPNPDLIDMAINDLIVEG--LLEEK-----LDSFNIPFT-----PSAE-----E 273  
 Db 879 NPLNCSTKVTYLTQALVYGCAMLSQTKCKHOLAVISSPVSTILNLGSPVVEYARRA 938  
 Oy 274 VKCIVEREGSCILLV-----ETFRAYHADAFAISID-----DYVRSHEQIKR 316  
 Db 939 IQCQALSGVAPFYLLIDHLISKAEEITSDAAYVYODLATFELQREKKLKHOKL-S 997  
 Oy 317 EYVASLIRSYE-----PILASHPEGAIMPLF-----HILAKHAA 352  
 Db 998 ETLKNILSCYVSPYIAKMDKMYLQGVNENVLSQLMLPMAOLLEKIQKPPYAVLKDER 1057  
 Oy 353 KYLHMGKGCYNNILSLAKKPKES 376  
 Db 1058 MYHLITLIGKINFEYSVLNEDPKS 1081

RESULT 5  
 ID POLG\_CXB3N STANDARD; PRT: 2185 AA.  
 AC P03133; 066322; 066323; 066324; 066325; 066326; 066327; 066328;  
 AC 083744;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1991 (Rel. 20, Last annotation update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Genome polypeptide [contains: Coat protein VP4 (P1A); Coat protein VP2  
 DE (P1B); Coat protein VP3 (P1C); Coat protein VP1 (P1D); Picornain 2A  
 DE (EC 3.4.22.25) (P2A); Core protein P2B; Core protein P2C; Core protein  
 DE P3A; Genome-linked protein VP6 (P3B); Picornain 3C (EC 3.4.22.28)  
 DE (Protease 3C) (P3C); RNA-directed RNA polymerase (EC 2.7.7.48) (P3D)].  
 DE Coxsackievirus B3 (strain Nancy).  
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Enterovirus.  
 ON NCBI\_TaxID=103903;  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=90204667; PubMed=2157045;  
 RA Klump W.M., Bergmann I., Mueller B.C., Amels D., Kandolf R.,  
 RT "Complete nucleotide sequence of infectious Coxsackievirus B3 CDNA:  
 RT two initial 5' uridine residues are regained during plus-strand RNA  
 RT synthesis."  
 RL J. Virol. 64:1573-1583(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=87122156; PubMed=3027968;  
 RA Lindberg A.M., Staalhanske P.O.K., Pettersson U.,  
 RT "Genome of coxsackievirus B3."  
 RL Virol. 156:50-63(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=84292451; PubMed=6088796;  
 RA Staalhanske P.O.K., Lindberg A.M., Pettersson U.,  
 RT "Replicase gene of coxsackievirus B3."  
 RL J. Virol. 51:742-746(1987).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 1-851.  
 RA Muehlbauer J.K., Kremer M., Minor I., Tong L., Zlotnick A.,  
 RA Johnson J.E., Rossmann M.G.;  
 RT "Structure determination of coxsackievirus B3 to 3.5-A resolution."  
 RL Acta Crystallogr. D 51:871-887(1995).  
 CC -1- FUNCTION: P2A AND THE P3C POLYPEPTIDES ARE PROTEASES THAT CLEAVE  
 CC AT CERTAIN O/G SITES IN THE POLYPROTEIN. THEY ARE CYSTEINE  
 CC PROTEASES.  
 CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR  
 CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.  
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS.  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -1- P1A: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC CLEAVAGE BETWEEN VP4 AND VP2 IS AUTOCATALYTIC; VP1/P2A IS  
 CC CATALYZED BY P2A; ALL OTHER CLEAVAGES ARE CATALYZED BY P3C.  
 CC -1- SIMILARITY: P2A PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC -1- SIMILARITY: P3C PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: M33854; AAA42931.1;  
 DR EMBL: K02709; AAA42932.1;  
 DR EMBL: M6572; AAA44400.1;  
 DR PIR: A26354; GNIB3.  
 DR PIR: A34664; GNIBT.  
 DR PDB: 1COV; 08-MAR-96.  
 DR MEROPS: C03.011;  
 DR MEROPS: C03.022;

DR InterPro: IPR000199; Cys-protease-3C.  
 DR InterPro: IPR000138; Pico\_P1A.  
 DR InterPro: IPR000081; Pico\_P2A.  
 DR InterPro: IPR002527; Pico\_P2B.  
 DR InterPro: IPR01205; RNA\_pol\_P3D.  
 DR InterPro: IPR001676; RV.  
 DR Pfam: PF00548; Cys-protease-3C; 1.  
 DR Pfam: PF02226; Pico\_P1A; 1.  
 DR Pfam: PF00947; Pico\_P2A; 1.  
 DR Pfam: PF01552; Pico\_P2B; 1.  
 DR Pfam: PF00073; RV; 3.  
 DR Pfam: PF00680; RNA\_dep\_RNA\_pol; 1.  
 DR ProDom: PD001125; Cys-protease-3C; 1.  
 DR ProDom: PD001274; Pico\_P2B; 1.  
 DR ProDom: PD001306; Pico\_P2A; 1.  
 DR Polyprotein: Coat protein; Core protein; Myristate; Hydrolyase; Thiol protease; 3D-structure.  
 DR RNA-directed RNA polymerase; 2.  
 DR CHAIN 70 69  
 FT CHAIN 2 332  
 FT CHAIN 333 570  
 FT CHAIN 571 851  
 FT CHAIN 852 1001  
 FT CHAIN 1002 1100  
 FT CHAIN 1101 1438  
 FT CHAIN 1439 1518  
 FT CHAIN 1519 1540  
 FT CHAIN 1541 1723  
 FT CHAIN 1724 2185  
 FT LIPID 2  
 FT ACI\_SITE 1687 1687  
 FT ACI\_SITE 1701 1701  
 FT ACI\_SITE 16 16  
 FT CONFLICT 177 177  
 FT CONFLICT 469 469  
 FT CONFLICT 487 487  
 FT CONFLICT 510 510  
 FT CONFLICT 516 516  
 FT CONFLICT 566 566  
 FT CONFLICT 593 593  
 FT CONFLICT 650 650  
 FT CONFLICT 854 854  
 FT CONFLICT 873 873  
 FT CONFLICT 1097 1097  
 FT CONFLICT 1280 1280  
 FT CONFLICT 1437 1437  
 FT CONFLICT 1503 1503  
 FT CONFLICT 1616 1616  
 FT CONFLICT 1624 1624  
 FT CONFLICT 1627 1627  
 FT CONFLICT 1630 1630  
 FT CONFLICT 1718 1718  
 FT CONFLICT 1734 1734  
 FT CONFLICT 1758 1758  
 FT CONFLICT 1824 1824  
 FT CONFLICT 1867 1867  
 FT CONFLICT 1880 1880  
 FT CONFLICT 2001 2001  
 FT CONFLICT 2095 2095  
 FT CONFLICT 2115 2115  
 FT CONFLICT 2175 2175  
 FT CONFLICT 2178 2178  
 FT SEQUENCE 2185 AA; 243451 MM; 1B5EC3D473386F CRC64;  
 Query Match 5.0%; Score 98; DB 1; Length 2185;  
 Best Local Similarity 19.2%; Pred. No. 15; Indels 90; Gaps 16;  
 Matches 73; Conservative 62; Mismatches 155; Indels 90; Gaps 16;  
 QY 1 MELQELVHMGEGDSTYAKNASTYLAKVPELEOCIRELLRANLPINRCIVADLG 60  
 DB 1818 MLEDAVYVGEGLDALDTTSAGYPAVALGIRK-----RRLSKTKLDTLKRCMDKRY 1871  
 QY 61 CASGPNTLTFVRDIWVOSIDKVGQEKNELEPRTIOIFLNDLFQNDNSYFKLLPSFYRKL 120

DB 1872 GLNLP-WTYKDELRSIEKVAKGRSLTEASSL-----NDSVAMRCFPGNLTXTF 1921  
 QY 121 EKENNRKIGSGLISAMPDSYGRLPPEESMHFLSCYSVHMLSOV-----SGLYELG 174  
 DB 1922 HLNPGVTVGSA-VCCPDLPFKSKIRPMLDGLHIAFDVSGYDALSLVYVACAKMLLELTG 1980  
 QY 175 ICANKGSTYSSKSGCRPPVCAKAIQDFTQDFTFLRHSKELFSGRMMLTCLCKDERDE 234  
 DB 1981 -----YTHK-----ETNYIDYLCNSHLY--RDKHYFVKGMPSCG----- 2014  
 QY 235 PNPDLDMALNDLIVEGLL-----EEREKLDSENIPEF-----TPSAEYKIVE---- 279  
 DB 2015 -SGTIFSMNNIITLTKYKIDIDQFRMAYGDVYASYPMPIDASLAEAGKG 2073  
 QY 280 -----EEGSC--ELTYLE-TFNAHYDAFISIDDDYPVRSHEQIKAEYVASLIRSYE 328  
 DB 2074 YGLIMTPADKCECENEVTWNTNATFLKRY---FRADEQYPLVHPVPMKDIESIRMTKD 2130  
 QY 329 P-----ILASHFGE 337  
 DB 2131 PKNTDHRSLCLAMHNGE 2150  
 RESULT 6  
 ID POLG\_EC09B STANDARD; PRT: 2203 AA.  
 AC 0665777  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 40, Last annotation update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Genome polyprotein [Contents: Coat protein VP4 (P1A); Coat protein VP2 (P1B); Coat protein VP3 (P1C); Coat protein VP1 (P1D); Picornain 2A (EC 3.4.22.29) (P2A); Core protein P2B; Core protein P2C; Core protein P2A; Genome-linked protein VPg (P3B); Picornain 3C (EC 2.7.7.48) (P3D)].  
 DE (P3A); Genome-linked protein VPg (P3B); Picornain 3C (EC 2.7.7.48) (P3D)].  
 DE Echovirus 9 (strain Barty).  
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Enterovirus.  
 NC NCBI\_Taxid-103914;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-9703384; Pubmed-8879131;  
 RX Zimmerman H., Eggers H.J., Neisen-Salz B.;  
 FT "Molecular cloning and sequence determination of the complete genome of the virulent echovirus 9 strain Barty."  
 FT Virus Genes 12:149-154(1996).  
 RL  
 CC 1- FUNCTION: P2A AND THE P3C POLYPEPTIDES ARE PROTEASES THAT CLEAVE AT CERTAIN C/G SITES IN THE POLYPROTEIN. THEY ARE CYSTEINE PROTEASES.  
 CC 1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2, VP3, AND VP4.  
 CC 1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC CLEAVAGE BETWEEN VP4 AND VP2 IS AUTOCATALYTIC; VP1/P2A IS CATALYZED BY P2A; ALL OTHER CLEAVAGES ARE CATALYZED BY P3C.  
 CC 1- SIMILARITY: P2A PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC 1- SIMILARITY: P3C PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC DB EMBL: X82886; CA63480.1;  
 CC DB HSSP: P21404; IDAM.  
 DR InterPro: IPR004004; Calicel\_pol\_hel.  
 DR InterPro: IPR000199; Cys-protease-3C.  
 DR InterPro: IPR00138; Pico\_P1A.  
 DR InterPro: IPR000081; Pico\_P2A.

```

0Y 42 LLAUPLINCKICVADLGCAGPMTLLVROIVOSIDVGOEKNELBEPITQIFLMDL 107
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 LINENGVAVLKNILKGRISYEMST-----DLPRVOYHGKFKLDRVYVCHMSLU 255
0Y 102 FONDNSYFKL-----LPSPYKLEKE-----NGRK 127
Db 254 QERDNNVNRKCNNEHEKNNNNNSLAVLQOLNINLILFQDDELEYLNKITSNGIL 313
0Y 128 IGSCI---ISANPGSFYGR---LEPESNHPLHSCYSVHMLSOVPSGLVTELGJANKG 180
Db 314 YDELLTLLNISSEKFKYFIKITSILNGKOFYFNSYV-----GGLIKIKYIMLSNGY 366
0Y 181 SIYS-SKSGCRP-----PYCKAVLDQFRKDEFTPLRHSKEFNS 217
Db 365 SEYNOSQTNPKLNGKPKTFPAIVYSKMKSSLEDLLNYSQLNKKDQSOIMLFSSNIMS 424
0Y 218 R-----GMLLTGICKVDEFEPPNLDLMA-----INLIV 250
Db 425 ESYTLKEVRNIMWTJPDPFSEQYNOILGSRISRFYSFOISKNPVYVLLAVYADDDOIT 488
0Y 251 EBLLEEKULSUF-IEFFPSAEVKICVIEEBSCHLYLTFPAKH-----YDAFASIDD 304
Db 485 S--LEDYSLEINTLFF-----DLK-----KLITLK-FTKETNRITSILONISD 528
0Y 305 DYPVASHQIKAEVYASLSRSY 327
Db 527 TRAMPPIYELVLEIVROPEF 549

```



AC P52519; 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Large structural phosphoprotein homolog (PPI00).  
GN U11.  
OS Human herpesvirus (type 7 / strain J1) (HHV7).  
OC Alphaherpesvirinae; Simplexvirus.  
OC NCBI\_TaxID=57278;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nicholas J.;  
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: TO THE LARGE STRUCTURAL PHOSPHOPROTEINS OF HSV-6 AND  
HCW UL32.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: U43400; AAC5672.1;  
DR Matrix protein; Phosphorylation.  
SQ SEQUENCE 755 AA; 86580 MW; 4083744CCCF91DA CRC64;  
  
Query Match 4.9%; Score 97; DB 1; Length 755;  
Best Local Similarity 19.8%; Pred. No. 4.2;  
Matches 73; Conservative 57; Mismatches 130; Indels 108; Gaps 16;  
  
QY 35 LEOCCRELLRLANPNKICIKVADLGASGPT-----LTVRDI----- 74  
DB 414 INQVIDTSLKIDLHNSKVIDI-----VSSPVNVVOLPKNKIDYHSTFLEPNEVNRON 468  
QY 75 -VQSIDKGOEKNELEL-----PTQIPIINDLFO-----NDEN 107  
DB 469 GVOSSDOLSKNSTNDLOKIELERIKIKONNEDIFLPESEKREIVHENLQSPDEH 528  
QY 108 SVFKLIPFVFKLEKNGRIGISCLAMPGSFVRLPESMFHLSGS----- 158  
DB 529 NEMSLPPODOKSIOKONKANS-----STTLKMITNOVNASMEKESASAKKNQVND 585  
QY 159 VHWLSQVSGVITELGANKGSITSK-----GCRPVQKAVLDQFKDPTTLRIHSKE 214  
DB 586 VKW---TPSSSLDL-----SRNDLQKELPESGLSEKVK-----LITDPTDTSLEERS 634  
QY 215 LFSRGRML-----TCICKVDEPDEPNPLDLLDINAINDLIVEGLLEEKLDSPNIFEPFP 269  
DB 635 L---KDLIEPPKTDVSNATATNDNNLNKLNKRKRDPLFQNSFTEKKQPVRSFFFLP 690  
QY 270 SAEVWCIYEESGCEILYETFKAHYDAFS-----IDDDYVRSHEQIKAE 317  
DB 691 NAE-----IOPFDSGLL-----TGKETONTIFGASKAQENGDKLDIDENSVCDDDIYVK 742  
QY 318 YVASLIRS 325  
DB 743 LVSHLTHS 750  
  
RESULT 9  
POLG\_SYDVH STANDARD; PRT; 2185 AA.  
ID POLG\_SYDVH  
AC P16604;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins  
DE P2A TO P2C; P3A; Genome-linked protein VPg; Picornain 3C  
DE (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D

DE (EC 2.7.7.48)).  
OS Swine vesicular disease virus (strain H/3 '76).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Enterovirus  
OX NCBI\_TaxID=12076;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=89279274; PubMed=2543767;  
RA Inoue T., Suzuki T., Sekiguchi K.;  
RL J. Gen. Virol. 70:919-934(1989).  
CC The complete nucleotide sequence of swine vesicular disease virus."  
CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR  
CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.  
CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN  
CC O/G SITES IN THE POLYPEPTIDE. IT MAY BE A CYSTEINE PROTEASE.  
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,  
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
CC VP3, AND VP4.  
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: D00435; BA00337.1;  
DR PIR: A1331; GNNYSH.  
DR HSSP: P21404; IDAM.  
DR MEROPS: C03.001; -;  
DR InterPro: IPR000199; Cys-protease-3C.  
DR InterPro: IPR003138; Pico\_P1A.  
DR InterPro: IPR000081; Pico\_P2B.  
DR InterPro: IPR002527; Pico\_P2B.  
DR InterPro: IPR000605; RNA\_helicase.  
DR InterPro: IPR001205; RNA\_pol\_P3D.  
DR InterPro: IPR001676; Rhv.  
DR Pfam: PF00548; Cys-protease-3C; 1.  
DR Pfam: PF02226; Pico\_P1A; 1.  
DR Pfam: PF00947; Pico\_P2A; 1.  
DR Pfam: PF01552; Pico\_P2B; 1.  
DR Pfam: PF00073; rhv\_3; 1.  
DR Pfam: PF00680; RNA\_dep\_RNA\_pol; 1.  
DR Pfam: PF00910; RNA\_helicase; 1.  
DR Pfam: PD001125; Cys-protease-3C; 1.  
DR Pfam: PD001306; Pico\_P2A; 1.  
DR Pfam: PD001306; Pico\_P2B; 1.  
KW Polyprotein; Coat protein; Core protein; Transferase;  
KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.  
FT CHAIN 2  
FT CHAIN 69  
FT CHAIN 70 330  
FT CHAIN 331 568  
FT CHAIN 569 851  
FT CHAIN 852 1001  
FT CHAIN 1002 1100  
FT CHAIN 1101 1429  
FT CHAIN 1430 1518  
FT CHAIN 1519 1540  
FT CHAIN 1541 1723  
FT CHAIN 1724 2185  
FT LIPID 2  
FT ACT\_SITE 1687 1687  
FT ACT\_SITE 1701 1701  
FT ACT\_SITE 2185 2185  
SQ SEQUENCE 2185 AA; 243164 MW; 582285DD9482B3B6 CRC64;  
  
Query Match 4.9%; Score 97; DB 1; Length 2185;  
Best Local Similarity 19.2%; Pred. No. 18;  
Matches 73; Conservative 62; Mismatches 155; Indels 90; Gaps 16;

```

OY 1 MELQEVLMHNEGGDTSYAKNASYMLALAKVPFLQECIRELLRANLPINKCKJAVDLG 60
DB 1818 MKLEDAVYGTGEJALDLTTSAGYVYALGIK-----RDLSKKTROLKLEKCDXY 1871
OY 61 CASGPNLLTVRDIYOSIDKVGQEKNELEPRTIQIFLNDLPQNDNSVFKLLPSFYKRL 120
DB 1872 GLNLP-VWTYVKDELMSAKVAKGKSRLEASSL-----NDSVAMROTFGNLTKTF 1921
OY 121 EKENGRKIGSCLSLAMPSEFYGRLEPESMHLFHSQSYHMLSQV-----SLVYELG 174
DB 1922 HLNPGIVTGA-VGCDPVDVFSKIFVMDGLHLPDLSGDASLSVWFTCLKLLEKLG 1980
OY 175 IGANKGSYSSKCCRPVOKAVLDQFTKDTFTFLRHSHKELFSRGMLLTCTICKVDEDE 234
DB 1981 -----YTNK-----ETNYIDLCSNHLV---RDKHYFVRGMPSGC----- 2014
OY 235 PNPLDLDMALNDLIVEGLL-----EERKLDSENIPEF-----TPSAEYKACIVE--- 279
DB 2015 -SGTISFNSMINIILRTLMKVKYKGLDQFRMAYGDDVIASYPWPIDASLAEAGKG 2073
OY 280 -----EEGSC--EILYLE-TFKAHYDAFSIDDYVRSHEQIKAEVYASLRSYVE 328
DB 2074 YGLIMTPADGECFENVTWNTVTLKRY---FRADQYFPLVHPVPMKDIHESIRMTKD 2130
OY 329 P-----TLASHFGE 337
DB 2131 PKNTQDHYVRSCLLAWHNCE 2150

RESULT 10
POLG_SVDVU STANDARD: PRT: 2185 AA
AC PI3900: 084794; 084795; 084796; 084797; 084798; 084799; 084800;
AC 084801; 084802; 084803; 084804;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polyprotein [contains: Coat proteins VP1 to VP4; Core proteins
DE P2A to P2C; P3A; Genome-linked protein VPg; Picornain 3C
DE (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D
DE (EC 2.7.7.48)].
OS Swine vesicular disease virus (strain UKG/27/72)..
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12077;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90364770; PubMed=2168111;
RA Seachurn P., Knowles N.J., McCauley J.W.;
RT "The complete nucleotide sequence of a pathogenic swine vesicular
RT disease virus."
RT Virus Res. 16:255-274 (1990).
CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR
CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.
CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PFM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL: X54521; CAA38377.1;
CC PIR: A30061; GNNYSV.

```

```

DR PIR: S11670; S11670.
DR HSSP: P03313; 1COV.
DR MEROPS: C03.001; -.
DR MEROPS: C03.020; -.
DR InterPro: IPR000199; Cys-protease-3C.
DR InterPro: IPR000138; Pico_P1A.
DR InterPro: IPR000081; Pico_P2A.
DR InterPro: IPR002527; Pico_P2B.
DR InterPro: IPR001676; RNV.
DR Pfam: PF00548; Cys-protease-3C; 1.
DR Pfam: PF02226; Pico_P1A; 1.
DR Pfam: PF00947; Pico_P2A; 1.
DR Pfam: PF01552; Pico_P2B; 1.
DR Pfam: PF00073; rhv; 3.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR ProDom: PD001125; Cys-protease-3C; 1.
DR ProDom: PD001274; Pico_P2B; 1.
DR ProDom: PD001306; Pico_P2A; 1.
DR Polyprotein: Coat protein; Core protein; Core protein; Transferase;
KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.
FT CHAIN 2 69
FT CHAIN 70 330
FT CHAIN 331 568
FT CHAIN 569 851
FT CHAIN 852 1001
FT CHAIN 1002 1100
FT CHAIN 1101 1429
FT CHAIN 1430 1518
FT CHAIN 1519 1540
FT CHAIN 1541 1723
FT CHAIN 1724 2165
FT LIPID 2
FT ACT_SITE 1687 1687
FT ACT_SITE 1701 1701
FT PROTEASE (POTENTIAL).
SQ SEQUENCE 2185 AA; 243363 MW; C9B103052934E1B8 CRC64;

Query Match 4.9%; Score 97; DB 1; Length 2185;
Best Local Similarity 19.2%; Pred. No. 18;
Matches 73; Conservative 62; Mismatches 155; Indels 90; Gaps 16;

OY 1 MELQEVLMHNEGGDTSYAKNASYMLALAKVPFLQECIRELLRANLPINKCKJAVDLG 60
DB 1818 MKLEDAVYGTGEJALDLTTSAGYVYALGIK-----RDLSKKTROLKLEKCDXY 1871
OY 61 CASGPNLLTVRDIYOSIDKVGQEKNELEPRTIQIFLNDLPQNDNSVFKLLPSFYKRL 120
DB 1872 GLNLP-VWTYVKDELMSAKVAKGKSRLEASSL-----NDSVAMROTFGNLTKTF 1921
OY 121 EKENGRKIGSCLSLAMPSEFYGRLEPESMHLFHSQSYHMLSQV-----SLVYELG 174
DB 1922 HLNPGIVTGA-VGCDPVDVFSKIFVMDGLHLPDLSGDASLSVWFTCLKLLEKLG 1980
OY 175 IGANKGSYSSKCCRPVOKAVLDQFTKDTFTFLRHSHKELFSRGMLLTCTICKVDEDE 234
DB 1981 -----YTNK-----ETNYIDLCSNHLV---RDKHYFVRGMPSGC----- 2014
OY 235 PNPLDLDMALNDLIVEGLL-----EERKLDSENIPEF-----TPSAEYKACIVE-- 279
DB 2015 -SGTISFNSMINIILRTLMKVKYKGLDQFRMAYGDDVIASYPWPIDASLAEAGKD 2073
OY 280 -----EEGSC--EILYLE-TFKAHYDAFSIDDYVRSHEQIKAEVYASLRSYVE 328
DB 2074 YGLIMTPADGECFENVTWNTVTLKRY---FRADQYFPLVHPVPMKDIHESIRMTKD 2130
OY 329 P-----TLASHFGE 337
DB 2131 PKNTQDHYVRSCLLAWHNCE 2150

RESULT 11
OPIAL_HUMAN

```

ID OPAL HUMAN STANDARD: PRT: 960 AA.  
AC 06013:  
DR 16-OCT-2001 (Rel. 40, Created)  
DR 16-OCT-2001 (Rel. 40, Last sequence update)  
DR 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Dynamn-like 120 kDa protein, mitochondrial precursor (Optic atrophy 1 gene protein).  
GN OPAL OR KIAA0567.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98290545; PubMed=9628581;  
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,  
RT "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."  
RL DNA Res. 5:31-39(1998).  
RN [2]  
RP SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND VARIANT OPAL GLO-300.  
RX MEDLINE=20472323; PubMed=11017079;  
RA Delattre C., Lederaers G., Griffoin J.-M., Gigarel N., Lorenzo C., Belenguer P., Pelloquin L., Grosgeorge J., Turc-Carel C., Perret E., Astarie-Dequeker C., Lasquellec L., Arnaud B., Duccommun B., Kaplan J., Hamel C.P.,  
RT "Nuclear gene OPAL, encoding a mitochondrial dynamn-related protein, is mutated in dominant optic atrophy."  
RL Nat. Genet. 26:207-210(2000).  
RN [3]  
RP TISSUE SPECIFICITY, AND VARIANTS OPAL GUN-290 AND ILE-432 DEL.  
RX MEDLINE=20472324; PubMed=11017080;  
RA Alexander C., Votruba M., Pesch U.E.A., Thiselton D.L., Mayer S., Moore A., Rodriguez M., Kellner U., Leo-Kottler B., Abuburger G., Bhattacharya S.S., Wistinger B.,  
RT "OPAL, encoding a dynamn-related GTPase, is mutated in autosomal dominant optic atrophy linked to chromosome 3q28."  
RL Nat. Genet. 26:211-215(2000).  
CC -1- FUNCTION: May be involved in mitochondrial biogenesis.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
CC -1- TISSUE SPECIFICITY: Highly expressed in retina. Also expressed in brain, testis, heart and skeletal muscle.  
CC -1- DISEASE: Defects in OPAL are a cause of optic atrophy type 1 (OPAL). OPAL is a dominantly inherited optic neuropathy occurring in 1 in 50,000 individuals that features progressive loss in visual acuity leading, in many cases, to legal blindness.  
CC -1- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL, AB011139; BAA25493.1;  
CC DR MIM: 605290;  
CC DR MIM: 165500;  
CC DR InterPro: IPR001401; Dynamln.  
CC DR Pfam: PF00350; dynamln.1.  
CC DR PRINTS: PR00195; DYNAMIN.  
CC DR SMART: SM00053; DYNC.1.  
CC KM Motor protein; GTP-binding; Mitochondrion; Transit peptide; Mitochondrial precursor; Vision.  
CC FT TRANSIT 1 2  
CC FT CHAIN 1 960 MITOCHONDRION (POTENTIAL)  
CC FT NP\_BIND 393 302 DYNAMIN-LIKE 120 KDA PROTEIN.  
CC FT NP\_BIND 398 402 GTP (POTENTIAL).  
CC FT NP\_BIND 467 470 GTP (POTENTIAL).

FT VARIANT 290 290 R -> Q (IN OPAL).  
FT FT /FTID-VAR\_011483.  
FT FT VARIANT 300 300 G -> E (IN OPAL).  
FT FT /FTID-VAR\_011484.  
FT FT VARIANT 432 432 MISSING (IN OPAL).  
FT FT /FTID-VAR\_011485.  
SO SEQUENCE 960 AA; 111657 MW; A3A943EC8664C538 CRC64;  
Query Match 4.9%; Score 96.5; DB 1; Length 960;  
Best Local Similarity 18.2%; Pred. No. 6.4;  
Matches 66; Conservative 60; Mismatches 123; Indels 113; Gaps 15;  
25 NLAAKVPFLEOCIRELRANLPINCKIVADLCASGPNLLTVYRDIYOSIVGOE 84  
DB 404 NVTSGMADPTKETETFSISKAYMNPALITLCTODSVDAERSIVT--DIVSQMDPHG-- 459  
QY 85 EKNELEPPTIOFELN-DLFONDFSVFKLPSFYRLEKENGRKIGSCLLSAMPGSFYGR 143  
DB 460 -----RRTIFVLTVDLAEKNVAS-----PSRIQI-----IEGR 489  
QY 144 LPPESMHFLHSCYVHMLSOVPSGLVIEIGICANKGSIYSKGCPRPVOKAIILOPTD 203  
DB 490 LFPKALGY-----FAVYTGKNSSESTEA----- 514  
QY 204 FTFELRHSKELFSRGRMLNLCICKYDEDEPNPDLIDMAINDLIVEGLE--EERLDS 261  
DB 515 ---IREYEFEFQNSKILKTSMLKAHQVTRN---LSLAVSDCFMKMYRESVEGOADS 566  
QY 262 FNIPFTPSAEVKIVIEEGSCETLYET-FKAHYDAFSDIDYFVSRHEDIKAEVYA 320  
DB 567 FKATRRN-----LETETKNYPRLEIDRN--ELFEKAKNEIID 603  
QY 321 SLIRSYVEPLIASHGEAIMPDLPRLAKHAQVLT-----MGKGCYNNLI-LSLAKRP 373  
DB 604 EVIS--LSQVTRKMHEDILQOSLMEKSTHVIENITLPAQGMNSGFNTTVIKIKMT 661  
QY 374 EK 375  
DB 662 DK 663  
RESULT 12  
OPAL MOUSE STANDARD: PRT: 960 AA.  
ID OPAL MOUSE  
AC P58281;  
DR 16-OCT-2001 (Rel. 40, Created)  
DR 16-OCT-2001 (Rel. 40, Last sequence update)  
DR 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Dynamn-like 120 kDa protein, mitochondrial precursor (Large GTP binding protein) (larger).  
GN OPAL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX Miyashita T., Misaka T., Kubo Y.,  
RT "Isolation of a cDNA for a novel large GTP-binding protein of the mouse brain."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: May be involved in mitochondrial biogenesis.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>



```

OY 121 EKENGKISGLISAMPSCFYGRFLPFEESMHFLHSCYSVHMLSGVP-----SGLVTEIG 174
DB 1920 HANPGLVYGS-A-VCCDDPLFMSKIPVMDLGHILRADISGIVASISPVWPAKLLLEKLG 1978
OY 175 IGANKGSIYSSKGRPVQAKYLDQFTKDTFFLRHSKELFSRGRMLLTCLCKVDEDE 234
DB 1979 -----YSKR-----ETNYIDYLCNSHMLY-----RDKHYFVGGMPSCG----- 2012
OY 235 PNPDLDMALINDLIVEGLI-----EERKLSFNIP----- 265
DB 2013 -SGTSIFNSMINIITIRLTFKFKYKIDIDQFRMAYGDDVIASYPPLIDASILAEAGKG 2071
OY 266 ---FTFPAEEKVICVEEGSC---ELIYLE-TEKHAHYDAFSIDDDVPVSHQIKAEVY 319
DB 2072 YGLIMTPA-----DKGECNELTWNVTFLKRY---FRADQYPLVHPVMPIDI 2119
OY 320 ASLIRSVPE-----ILASHGEALIMPD.FHRL 347
DB 2120 HESIRWTDPKNTGYHVRSLCLAMHNGEYEEELTPKT 2158

RESULT 14
POLG_EC30B STANDARD; PRT: 2194 AA.
ID POLG_EC30B
AC 09MNT8;
DT 01-MAR-2002 (Rel. 41, last sequence update)
DT 01-MAR-2002 (Rel. 41, last annotation update)
DE Genome polypeptide [Contains: Coat protein VP1 (P1a); Coat protein VP2 (P1b); Coat protein VP3 (P1c); Coat protein VP4 (P1d); Picornain 2A (EC 3.4.22.29) (P2a); Core protein P2B; Core protein P2C; Core protein P3A; Genome-linked protein VPg (P3B); Picornain 3C (EC 3.4.22.28) (P3D); Echovirus 30 (strain Bastian)]
DE Picornaviruses: ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus;
OX NCBI_taxid-176284;
RN NCBI_taxid-176284;
RA Zell R.;
RT "Complete genome of echovirus 30 strain Bastian."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: P2A AND THE P3C POLYPEPTIDES ARE PROTEASES THAT CLEAVE AT CERTAIN O/G SITES IN THE POLYPEPTIDE. THEY ARE CYSTEINE PROTEASES (BY SIMILARITY).
CC -1- FUNCTION: It is thought that the P2C protein attaches to vesicular membranes and is associated with viral RNA synthesis (By similarity).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2, VP3, AND VP4 (BY SIMILARITY).
CC -1- PPM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS. CLEAVAGE BETWEEN VP4 AND VP2 IS AUTOCATALYTIC. VP1/P2A IS CATALYZED BY P2A; ALL OTHER CLEAVAGES ARE CATALYZED BY P3C (BY SIMILARITY).
CC -1- SIMILARITY: P2A PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -1- SIMILARITY: P3C PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL-outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by... and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL: AF162711; AAD45119.1;
DB InterPro: IPR004004; Calici.pol.bel.
DB InterPro: IPR000199; Cys-protease-3C.
DB InterPro: IPR000138; Pico_P1A.
DB InterPro: IPR000081; Pico_P2A.
DB InterPro: IPR002527; Pico_P2B.

```

```

DR InterPro: IPR001676; Rhv.
DR InterPro: IPR006059; RNA_helicase.
DR InterPro: IPR001205; RNA_pol.p3d.
DR Pfam: PF00548; Cys-protease-3C; 1.
DR Pfam: PF02226; Pico_P1A; 1.
DR Pfam: PF00947; Pico_P2A; 1.
DR Pfam: PF01552; Pico_P2B; 1.
DR Pfam: PF00073; Rhv; 3.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR Pfam: PF00910; RNA_helicase; 1.
DR PRINTS: PR00918; CALICIVIRUSNS.
DR ProDom: PD001125; Cys-protease-3C; 1.
DR ProDom: PD001274; Pico_P2B; 1.
DR ProDom: PD001306; Pico_P2A; 1.
KW Polyprotein; Coat protein; Core protein; Core protein; Transferase; Myristate;
KW RNA-directed RNA polymerase; Hydrolyase; Thiol protease.
FT CHAIN 2 69 COAT PROTEIN VP4.
FT CHAIN 70 330 COAT PROTEIN VP2.
FT CHAIN 331 588 COAT PROTEIN VP3.
FT CHAIN 589 860 COAT PROTEIN VP1.
FT CHAIN 861 1010 PICORNAIN 2A.
FT CHAIN 1011 1109 CORE PROTEIN P2B.
FT CHAIN 1110 1438 CORE PROTEIN P2C.
FT CHAIN 1439 1527 CORE PROTEIN P3A.
FT CHAIN 1528 1549 GENOME-LINKED PROTEIN VPg.
FT CHAIN 1550 1732 PICORNAIN 3C.
FT CHAIN 1733 2194 PICORNAIN 3C.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT ACT SITE 1696 1696 MYRISTATE 3C (POTENTIAL).
FT ACT SITE 1710 1710 PROTEASE 3C (POTENTIAL).
FT SEQUENCE 2194 AA; 245143 MW; F5944CEB091DC9AA CRC64;

```

Query Match 4.98; Score 96; DB 1; Length 2194;  
 Best Local Similarity 19.28; Pred. No. 21;  
 Matches 73; Conservative 61; Mismatches 156; Indels 90; Gaps 16;

```

OY 1 MELQEVLMHNEGSGDTSTAKNASTNLAKVPELEOCIRELLRANLPINKIKYADIG 60
DB 1927 MKLEDVAVTGETLEALDITTSAGYPVALGIRK-----RDLSKRTKDLAKKECDKRY 1880
OY 61 CASGPTLLTLDIVDIQSIDKVGQEKNELEPTIOTFLNDFONDFNSVERKLPSFRYL 120
DB 1881 GLNLP-MVYVYVDEHRSKAKVAKGKSLTEASL-----NDVAMROTGNLYKTF 1930
OY 121 EKENGKISGLISAMPSCFYGRFLPFEESMHFLHSCYSVHMLSGVP-----SGLVTEIG 174
DB 1931 HANPGLVYGS-A-VCCDDPLFMSKIPVMDLGHILRADISGIVASISPVWPAKLLLEKLG 1989
OY 175 IGANKGSIYSSKGRPVQAKYLDQFTKDTFFLRHSKELFSRGRMLLTCLCKVDEDE 234
DB 1990 -----YSKR-----ETNYIDYLCNSHMLY-----RDKHYFVGGMPSCG----- 2023
OY 235 PNPDLDMALINDLIVEGLI-----EERKLSFNIPF-----TPSAEEKVICVE 279
DB 2024 -SGTSIFNSMINIITIRLTFKFKYKIDIDQFRMAYGDDVIASYPPLIDASILAEAGKG 2082
OY 280 -----EGSC-ELIYLE-TEKHAHYDAFSIDDDVPVSHQIKAEVYASLISYVE 328
DB 2083 YGLIMTPADKGCFFNEVMTWVTFKRY---FRADQYPLVHPVMPMDIHESIRWTD 2139
OY 329 P-----ILASHGE 337
DB 2140 PKNTQDHVSRSLCLAMHNGE 2159

RESULT 15
POLG_CXA9 STANDARD; PRT: 2201 AA.
ID POLG_CXA9
AC P21404;
DT 01-MAY-1991 (Rel. 18, last sequence update)
DT 01-MAY-1991 (Rel. 18, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)

```

DE Genome polypeptide (contains: Coat protein VP4 (P1A); Coat protein VP2  
 DE (P1B); Coat protein VP3 (P1C); Coat protein VP1 (P1D); Core protein  
 DE P2A; Core protein P2B; Core protein P2C; Core protein P3A; Genome-  
 DE linked protein VP6 (P3B); Picornain 3C (EC 3.4.22.28) (Protease 3C)  
 DE (P3C); RNA-directed RNA polymerase (EC 2.7.7.48) (P3D)].  
 OS Coxsackievirus A9 (strain G1993).  
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 OC Enterovirus.  
 NC NCBL:TaxID=12068;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90111704; PubMed=2558158;  
 RA Chang K.H., Aavinen P., Hyypia T., Stanway G.,  
 RT The nucleotide sequence of coxsackievirus A9: implications for  
 RT receptor binding and enterovirus classification.";  
 RL J. Gen. Virol. 70:3269-3280(1989).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 1-870.  
 RX MEDLINE=20113480; PubMed=10647183;  
 RA Hendry E., Hatanaka H., Fry E., Smyth M., Tate J., Stanway G.,  
 RA Santti J., Maronen M., Hyypia T., Stuart D.,  
 RT "The crystal structure of coxsackievirus A9: new insights into the  
 RT uncoating mechanisms of enteroviruses.";  
 RL Structure 7:1527-1538(1999).  
 CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR  
 CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.  
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN  
 CC O/G SITES IN THE POLYPEPTIDE. IT MAY BE A CYSTEINE PROTEASE.  
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS.  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -1- PFM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VITRO YIELD NATURE PROTEINS.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by, and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL: D00627; BAA00518.1;  
 DR PIR: J00523; GNNVA9.  
 DR PDB: 1D4M; 23-DEC-99.  
 DR MEROPS: C03.022;  
 DR InterPro: IPR000199; Cys-protease-3C.  
 DR InterPro: IPR000138; Pico\_P1A.  
 DR InterPro: IPR000081; Pico\_P2A.  
 DR InterPro: IPR002527; Pico\_P2B.  
 DR InterPro: IPR000605; RNA\_helicase.  
 DR InterPro: IPR001205; RNA\_pol\_P3D.  
 DR InterPro: IPR001676; Rny.  
 DR Pfam: PF00548; Cys-protease-3C; 1.  
 DR Pfam: PF02226; Pico\_P1A; 1.  
 DR Pfam: PF00947; Pico\_P2A; 1.  
 DR Pfam: PF01552; Pico\_P2B; 1.  
 DR Pfam: PF00073; Rny; 3.  
 DR Pfam: PF00680; RNA\_dep\_RNA\_pol; 1.  
 DR Pfam: PF00910; RNA\_helicase; 1.  
 DR Pfam: PD001125; Cys-protease-3C; 1.  
 DR ProDom: PD001274; Pico\_P2B; 1.  
 DR ProDom: PD001306; Pico\_P2A; 1.  
 DR PolyProtein: Coat protein; Core protein; Transferase; 3D-structure;  
 KM RNA-directed RNA polymerase; Hydrolyase; Thiol protease; Myristate.  
 FT CHAIN 2 69 COAT PROTEIN VP4.  
 FT CHAIN 70 330 COAT PROTEIN VP2.  
 FT CHAIN 331 568 COAT PROTEIN VP3.  
 FT CHAIN 569 870 COAT PROTEIN VP1.  
 FT CHAIN 871 1017 CORE PROTEIN P2A.  
 FT CHAIN 1018 1116 CORE PROTEIN P2B.  
 FT CHAIN 1117 1445 CORE PROTEIN P2C.

Query Match	Similarity	Score	DB 1	Length	2201
Best Local	73	Conservative	62	Mismatches	155
Matches	73	Conservative	62	Mismatches	155
DB	1	MEDLINE=90111704; PubMed=2558158;	1	1446	1534
DB	1834	MEDLINE=90111704; PubMed=2558158;	1834	1446	1534
DB	61	CASGPTLLTVRDIVSISDKVGOEENKLEPTIQLFNDLFONDENVFKLLPSFYKRL	61	1446	1534
DB	1888	GLNLP-MITVYKQDLRSEAKVAKGKSLIEASSL-----NDSVAMRQTFGNLYKTF	1888	1446	1534
DB	121	EKENGRKIGSCLISAMPSPYGRHPPEESMHFLHSCSYVHMLSQVP-----SGLVIELG	121	1446	1534
DB	1938	HLNPGIVTGA-VGCDPDLFWKRPVLMGLHAFDYSXDASISPVWFCCLKLLEKIG	1938	1446	1534
DB	175	IGANGSIYSKGCGRPPYOKAYIDOFKTFPLIRHSEKELFSGKMLTLCICKVDEDE	175	1446	1534
DB	1997	-----YSHK-----ETNYIDLCNSHLX---RDKHYFRGGMPSGC-----	1997	1446	1534
DB	235	PAPLDLDMALINDIYVGLL-----EEKIDSPNIPF-----TSAEVCYIE-----	235	1446	1534
DB	2031	-SGTIFNSMNNIITLTKLKYKIGDIDDFMTATGDDVYASTPMDASLILAKKD	2031	1446	1534
DB	280	-----EEGSC--ETLYLE--TEKAHYDAFSIDDDPYRSHQIKAEVASLIRSYE	280	1446	1534
DB	2090	YGLIMTPADKCECPNEVTWNTVFLKRY---FRADQYPLVHPVPMKDIHESWTKD	2090	1446	1534
DB	329	P-----ILASHFGE 337	329	1446	1534
DB	2147	PNTQDHYRSLCLLAWHNGE 2166	2147	1446	1534

Search completed: July 27, 2002, 05:47:03  
 Job time: 414 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: July 27, 2002, 05:34:04 : Search time 62.29 Seconds  
(without alignments)  
1049.801 Million cell updates/sec

Title: US-09-971-020-1  
1972  
Sequence: 1 MELOEVLHNMEGEDTSYAK.....KGCYNLIISLAKPKESDV 378

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea:.\*  
2: SP bacteria:.\*  
3: SP fungi:.\*  
4: SP human:.\*  
5: SP invertebrate:.\*  
6: SP mammal:.\*  
7: SP mhc:.\*  
8: SP organelle:.\*  
9: SP phage:.\*  
10: SP plant:.\*  
11: SP rodent:.\*  
12: SP virus:.\*  
13: SP vertebrate:.\*  
14: SP unclassified:.\*  
15: SP rylus:.\*  
16: SP bacteriophage:.\*  
17: SP archaea:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	1972	100.0	09AVJ9	Q9AVJ9 coffee arab
2	1632	82.8	09AVK0	Q9AVK0 coffee arab
3	1593.5	80.8	09AVK1	Q9AVK1 coffee arab
4	1569.5	79.6	09AVL9	Q9AVL9 coffee arab
5	723.5	36.7	09AVR1	Q9AVR1 stephanotis
6	689	34.9	09AVG9	Q9AVG9 atropa bell
7	662.5	33.6	09S8K6	Q9S8K6 brassica ra
8	649.5	33.0	09SPV4	Q9SPV4 clarkia bre
9	649.5	32.9	09FYV9	Q9FYV9 anilinum
10	639	32.4	09AR07	Q9AR07 arabidopsis
11	635.5	32.2	09LR05	Q9LR05 arabidopsis
12	633	32.1	09FR76	Q9FR76 arabidopsis
13	629	31.8	09IS20	Q9IS20 arabidopsis
14	628	31.8	09FZM8	Q9FZM8 camellia
15	614.5	31.2	09CA39	Q9CA39 arabidopsis
16	586	29.7	09CA39	Q9CA39 arabidopsis

17	577.5	29.3	359	10	Q92PT3	Q92PT3 arabidopsis
18	526.5	26.7	378	10	Q943A3	Q943A3 oryza sativ
19	523	26.5	323	10	Q9FMR8	Q9FMR8 arabidopsis
20	459	23.3	380	10	Q9FWJ1	Q9FWJ1 oryza sativ
21	451	22.9	351	10	Q93XW1	Q93XW1 brassica ca
22	445.5	22.6	352	10	Q9RND0	Q9RND0 arabidopsis
23	439	22.3	351	10	Q9X157	Q9X157 arabidopsis
24	432	21.9	359	10	Q9FLN8	Q9FLN8 arabidopsis
25	425	21.6	353	10	Q9SL10	Q9SL10 arabidopsis
26	423.5	21.5	363	10	Q9C9W8	Q9C9W8 arabidopsis
27	416.5	21.1	374	10	Q9FCR8	Q9FCR8 arabidopsis
28	413.5	21.0	352	10	Q9C9M4	Q9C9M4 arabidopsis
29	411.5	20.9	619	10	Q9S592	Q9S592 arabidopsis
30	404.5	20.5	379	10	Q9FYC3	Q9FYC3 arabidopsis
31	401	20.3	348	10	Q9FYC6	Q9FYC6 arabidopsis
32	400	20.3	348	10	Q949P9	Q949P9 arabidopsis
33	396	20.1	353	10	Q9M4F2	Q9M4F2 brassica na
34	392.5	19.9	353	10	Q9C9M3	Q9C9M3 arabidopsis
35	392	19.9	353	10	Q93YL7	Q93YL7 brassica na
36	387.5	19.7	353	10	Q9C9M2	Q9C9M2 arabidopsis
37	387	19.6	353	10	Q9FXR0	Q9FXR0 arabidopsis
38	385	19.5	361	10	Q9FMA2	Q9FMA2 arabidopsis
39	373.5	18.9	358	10	Q9FTJ3	Q9FTJ3 brassica na
40	360	18.3	318	10	Q941F2	Q941F2 arabidopsis
41	198.5	10.1	210	10	Q98QW7	Q98QW7 mycoplasma
42	127.5	6.5	534	16	Q95919	Q95919 saccharomyc
43	107.5	6.0	439	17	Q9Y914	Q9Y914 aetopyrum p
44	107.5	5.5	999	17	Q95914	Q95914 aetopyrum p
45	106.5	5.4	585	4	Q965X5	Q965X5 homo sapien

## ALIGNMENTS

RESULT 1  
ID 09AVJ9 PRELIMINARY; PRT; 378 AA.  
AC 09AVJ9;  
DT 01-JUN-2001 (TREMUR1, 17, Created)  
DT 01-JUN-2001 (TREMUR1, 17, Last sequence update)  
DT 01-DEC-2001 (TREMUR1, 19, Last annotation update)  
DE 7-METHYLMETHYLTRANSFERASE.  
GN CAMANT.  
OS Coffea arabica (Coffee).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Asteridiales; euasterids I; Gentianales; Rubiaceae; Ixoroideae; Coffeae;  
OC Coffea.  
OX NCBI\_TaxID=13443;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, CATURRA;  
RX MEDLINE=2169383; PubMed=11108716;  
RA Ogawa M., Heral Y., Kozumi N., Kusano T., Sano H.;  
RT AND ENZYMOLOGICAL PROPERTIES OF THE METHYLMETHYLTRANSFERASE OF COFFEE PLANTS. GENE ISOLATION  
RT J. Biol. Chem. 276:8213-8218(2001).  
RL EMBL: AB048794; BAB9216.1;  
KW Transference; Methyltransferase.  
SQ SEQUENCE 378 AA; 42747 MW; F36184F3D5243809 CRC64;

Query Match 100.0%; Score 1972; DB 10; length 378;  
Best local similarity 100.0%; Pred. No. 2, 1e-161;  
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELOEVLHNMEGEDTSYAKASYNLAKVPPLEOCIRRELLRANPNINKIKYADG 60  
DB 1 MELOEVLHNMEGEDTSYAKASYNLAKVPPLEOCIRRELLRANPNINKIKYADG 60  
QY 61 CASGPTLITVADIVOSIDKVGDEKNELEFRTIOLFNDLFDNDPSVKKLPSYRKL 120  
DB 61 CASGPTLITVADIVOSIDKVGDEKNELEFRTIOLFNDLFDNDPSVKKLPSYRKL 120

QY 121 EKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 180  
DB 121 EKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 180  
QY 181 SIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 240  
DB 181 SIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 240  
QY 241 LDMALNDLIVEGLEEEKLDSFNIPFTPSAEVKCIVEEGSCIELYLETFAKHYDAF 300  
DB 241 LDMALNDLIVEGLEEEKLDSFNIPFTPSAEVKCIVEEGSCIELYLETFAKHYDAF 300  
QY 301 SIDDYVPSHEDQIRAEVVASLIRSYVEPIILASHGEALIMPOLFRILAKHAKVILHNGK 360  
DB 301 SIDDYVPSHEDQIRAEVVASLIRSYVEPIILASHGEALIMPOLFRILAKHAKVILHNGK 360  
QY 361 GYNNLIISLAKKPEKSDV 378  
DB 361 GYNNLIISLAKKPEKSDV 378

## RESULT 2

ID Q9AVK0 PRELIMINARY; PRT; 372 AA.  
AC Q9AVK0;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE THEOBROMINE SYNTHASE.  
GN CAMT3.  
OS Coffea arabica (Coffee).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; eunasterids I; Gentianales; Rubiaceae; Ixoroideae; Coffeae;  
OC Coffea.  
OX NCBI\_TaxID=13443;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CY. CATURRA;  
RX MEDLINE=21269383; PubMed=11108716;  
RA Ogawa M., Herai Y., Kozsumi N., Kusano T., Sano H.;  
RT \*7-Methylxanthine Methyltransferase of Coffee Plants. GENE ISOLATION  
AND ENZYMATIC PROPERTIES.  
RL J. Biol. Chem. 276:8213-8218(2001).  
DR EMBL; AB048793; BAB39215.1;  
SQ SEQUENCE 372 AA; 41842 MW; 1C9D2D53263828D2 CRC64;

Query Match 82.8%; Score 1632; DB 10; Length 372;  
Best Local Similarity 84.7%; Pred. No. 3.5e-132;  
Matches 321; Conservative 16; Mismatches 34; Indels 8; Gaps 2;

QY 1 MELOEVLHNMGECDTSYAKNASYN-LALAKVRFLEOCIRELIRANLPINIKCIRYADL 59  
DB 1 MELOEVLHNMGECDTSYAKNASYN-LALAKVRFLEOCIRELIRANLPINIKCIRYADL 59  
QY 60 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 119  
DB 60 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 119  
QY 61 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 120  
DB 61 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 120  
QY 120 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 179  
DB 120 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 179  
QY 121 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 180  
DB 121 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 180  
QY 180 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 239  
DB 180 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 239  
QY 181 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 240  
DB 181 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 240  
QY 240 LDMALNDLIVEGLEEEKLDSFNIPFTPSAEVKCIVEEGSCIELYLETFAKHYDAF 299  
DB 240 LDMALNDLIVEGLEEEKLDSFNIPFTPSAEVKCIVEEGSCIELYLETFAKHYDAF 299  
QY 361 GYNNLIISLAKKPEKSDV 378  
DB 361 GYNNLIISLAKKPEKSDV 378

QY 300 FSIDDYVPSHEDQIRAEVVASLIRSYVEPIILASHGEALIMPOLFRILAKHAKVILHNGK 359  
DB 300 FSIDDYVPSHEDQIRAEVVASLIRSYVEPIILASHGEALIMPOLFRILAKHAKVILHNGK 359  
QY 360 GYNNLIISLAKKPEKSDV 378  
DB 360 GYNNLIISLAKKPEKSDV 378

## RESULT 3

ID Q9AVK1 PRELIMINARY; PRT; 385 AA.  
AC Q9AVK1;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE THEOBROMINE SYNTHASE.  
GN CAMT3.  
OS Coffea arabica (Coffee).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; eunasterids I; Gentianales; Rubiaceae; Ixoroideae; Coffeae;  
OC Coffea.  
OX NCBI\_TaxID=13443;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CY. CATURRA;  
RX MEDLINE=21269383; PubMed=11108716;  
RA Ogawa M., Herai Y., Kozsumi N., Kusano T., Sano H.;  
RT \*7-Methylxanthine Methyltransferase of Coffee Plants. GENE ISOLATION  
AND ENZYMATIC PROPERTIES.  
RL J. Biol. Chem. 276:8213-8218(2001).  
DR EMBL; AB048792; BAB39214.1;  
SQ SEQUENCE 385 AA; 43270 MW; 92103A20A001B0E CRC64;

Query Match 80.8%; Score 1593.5; DB 10; Length 385;  
Best Local Similarity 81.3%; Pred. No. 7.6e-129;  
Matches 313; Conservative 25; Mismatches 40; Indels 7; Gaps 2;

QY 1 MELOEVLHNMGECDTSYAKNASYN-LALAKVRFLEOCIRELIRANLPINIKCIRYADL 59  
DB 1 MELOEVLHNMGECDTSYAKNASYN-LALAKVRFLEOCIRELIRANLPINIKCIRYADL 59  
QY 60 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 119  
DB 60 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 119  
QY 61 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 120  
DB 61 GCASGPTLLTFVADYOSIDKVGGEKNELEPRTIOIFLNDLFONDENSVFKLLPSFYRK 120  
QY 120 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 179  
DB 120 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 179  
QY 121 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 180  
DB 121 LEKENGRKISGLISAMPSEFYGRLEPPESSMHFLHSCSYVHMLSOVPSGLVIELGIGANK 180  
QY 180 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 239  
DB 180 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 239  
QY 181 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 240  
DB 181 GSIIYSSKGRPPVOKAYLDQFTKDFTLRIHSEKLEFSRGRMLLTICICVDFDEPNPLD 240  
QY 240 LDMALNDLIVEGLEEEKLDSFNIPFTPSAEVKCIVEEGSCIELYLETFAKHYDAF 299  
DB 240 LDMALNDLIVEGLEEEKLDSFNIPFTPSAEVKCIVEEGSCIELYLETFAKHYDAF 299  
QY 300 FSIDDYVPSHEDQIRAEVVASLIRSYVEPIILASHGEALIMPOLFRILAKHAKVILHNGK 353  
DB 300 FSIDDYVPSHEDQIRAEVVASLIRSYVEPIILASHGEALIMPOLFRILAKHAKVILHNGK 353  
QY 354 VLHMGKGYNNLIISLAKKPEKSDV 378  
DB 354 VLHMGKGYNNLIISLAKKPEKSDV 378  
QY 361 GYNNLIISLAKKPEKSDV 385  
DB 361 GYNNLIISLAKKPEKSDV 385

RESULT 4  
ID Q9AVL9 PRELIMINARY; PRT; 385 AA.  
AC Q9AVL9;



DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE CAFFEINE SYNTHASE.  
 GN CMTLL.  
 OS Coffea arabica (Coffee).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Gentianales; Rubiaceae; Ixoroidae; Coffeae;  
 OC Coffea.  
 NCBI\_TaxID=13443;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=CALLUS;  
 RX MEDLINE=21269383; PubMed=11108716;  
 RA Ogawa M., Heral Y., Koizumi N., Kusano T., Sano H.;  
 RT "7-Methylxanthine Methyltransferase of Coffee Plants. GENE ISOLATION  
 RT AND ENZYMATIC PROPERTIES."  
 RL J. Biol. Chem. 276:8213-8218(2001).  
 DR EMBL; AB039725; BAB39213.1;  
 SO SEQUENCE 385 AA; 43242 MW; 003A5837F0AE300 CRC64;

Query Match 79.6%; Score 1569.5; DB 10; Length 385;  
 Best Local Similarity 80.3%; Pred. No. 8; Be-127;  
 Matches 309; Conservative 26; Mismatches 43; Indels 7; Gaps 2;

OY 1 MELQEVLMHNGEGDSTYAKNASYN-LALAKYKPLEDCIRELLRANLPINKCIKIVADL 59  
 DB 1 MELQEVLMHNGEGDSTYAKNASYN-LALAKYKPLEDCIRELLRANLPINKCIKIVADL 60  
 OY 60 GCASGPNLTLLTVRDIVOSIDKVGQEKNELEPTQIFLNDLFONDNSVFKLLPSFYRK 119  
 DB 61 GCASGPNLTLLTVRDIVOSIDKVGQEKNELEPTQIFLNDLFONDNSVFKLLPSFYRK 120  
 OY 120 LEKENGKRGISCLISAMPSEFYGRLEPESMHFLHSCSYVHMLSOVPSGLVLELGIGANK 179  
 DB 121 LEKENGKRGISCLISAMPSEFYGRLEPESMHFLHSCSYVHMLSOVPSGLVLELGIGANK 180  
 OY 180 GSIVSSKCRPPVOKATLOFTKDFTLRIHSEKLEPESMHFLHSCSYVHMLSOVPSGLVLELGIGANK 239  
 DB 181 GSIVSSKCRPPVOKATLOFTKDFTLRIHSEKLEPESMHFLHSCSYVHMLSOVPSGLVLELGIGANK 240  
 OY 240 LLDMAINDLYEGLLEEKLDSEFNIPFTSPAEKCIYEESGCELYLETFKHAHYDA 299  
 DB 241 LLDMAINDLYEGLLEEKLDSEFNIPFTSPAEKCIYEESGCELYLETFKHAHYDA 300  
 OY 300 PSIDDDCVRRSHSPVSDERARAHAVALIRSYVEPIASHFGEALMPDLFRLAKNAK 353  
 DB 301 PSIDDDCVRRSHSPVSDERARAHAVALIRSYVEPIASHFGEALMPDLFRLAKNAK 360  
 OY 354 VLMHGKGCYNNLLIISLAKKPEKSDV 378  
 DB 361 VLMHGKGCYNNLLIISLAKKPEKSDI 385  
 RESULT 5  
 O9AVR1 PRELIMINARY; PRT; 366 AA.  
 AC O9AVR1.  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE S-ADENOSYL-L-METHIONINE: SALICYLIC ACID CARBOXYL  
 DE METHYLTRANSFERASE.  
 GN SAMT.  
 OS Stephanotis floribunda.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae;  
 OC Ceropetalaceae; Stephanotis.  
 NCBI\_TaxID=85838;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Pott M.B., Pichersky E., Plechulla B.;  
 RT "Circadian oscillation of methyl salicylate emission, samt enzyme  
 RT activity, and samt mRNA in flowers of Stephanotis floribunda."  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ308570; CAC33768.1;  
 SO SEQUENCE 366 AA; 41316 MW; 8D5675AB153F88BD CRC64;

Query Match 36.7%; Score 723.5; DB 10; Length 366;  
 Best Local Similarity 42.7%; Pred. No. 4; Be-54;  
 Matches 164; Conservative 64; Mismatches 125; Indels 31; Gaps 10;

OY 1 MELQEVLMHNGEGDSTYAKNASYN-LALAKYKPLEDCIRELLRANLPINKCIKIV 56  
 DB 1 MELQEVLMHNGEGDSTYAKNASYN-LALAKYKPLEDCIRELLRANLPINKCIKIV 54  
 OY 57 ADIGCASGPNLTLLTVRDIVOSIDKVGQEKNELEPTQIFLNDLFONDNSVFKLLP 114  
 DB 58 ADIGCASGPNLTLLTVRDIVOSIDKVGQEKNELEPTQIFLNDLFONDNSVFKLLP 110  
 OY 115 SFYRKLKENGKRGISCLISAMPSEFYGRLEPESMHFLHSCSYVHMLSOVPSGLVLELG 174  
 DB 111 SFYRKLKENGKRGISCLISAMPSEFYGRLEPESMHFLHSCSYVHMLSOVPSGLVLELG 165  
 OY 175 IGANKSIYSSKCRPPVOKATLOFTKDFTLRIHSEKLEPESMHFLHSCSYVHMLSOVPSGLVLELG 231  
 DB 176 IGANKSIYSSKCRPPVOKATLOFTKDFTLRIHSEKLEPESMHFLHSCSYVHMLSOVPSGLVLELG 224  
 OY 232 -FDEPNLDLMAINDLYEGLLEEKLDSEFNIPFTSPAEKCIYEESGCELYLE 290  
 DB 225 GRESGVALLELLRANLNEVLSGQLEEQDLCFVNPQYTPSPAEKCIYEESGCELYLE 284  
 OY 291 TFKAHYDAFISIDDDYVRRSHDQIK--AEYVSLIRSYVEPIASHFGEALMPDLFRLA 348  
 DB 285 ATTTHHTA--VDHGHVGHCHHAFKDCGYSLSNCRVAVPELVVHFGAALMDEVFHYR 341  
 OY 349 KHAQVLMHGKGCYNNLLIISLAKK 372  
 DB 342 ELLNCGTKEKIEFIVVSMKR 365

RESULT 6  
 O9AVG9 PRELIMINARY; PRT; 357 AA.  
 AC O9AVG9.  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE S-ADENOSYL-L-METHIONINE: SALICYLIC ACID CARBOXYL  
 DE METHYLTRANSFERASE.  
 GN ABSAMT.  
 OS Atropa belladonna (belladonna).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Atropa.  
 NCBI\_TaxID=33113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M8; TISSUE=ROOT;  
 RA Fukami H., Asakura T., Hirano H., Abe K., Shimomura K., Yamakawa T.;  
 RT "Cloning and expression of salicylic acid inducible and active S-  
 RT adenosyl-L-methionine:salicylic acid carboxyl methyltransferase in  
 RT transformed root culture of Atropa belladonna."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB049752; BAB39396.1;  
 SO SEQUENCE 357 AA; 40678 MW; FA6A1738FA967EF2 CRC64;

Query Match 34.9%; Score 689; DB 10; Length 357;  
 Best Local Similarity 42.0%; Pred. No. 4; Be-51;  
 Matches 161; Conservative 68; Mismatches 116; Indels 38; Gaps 10;

```

OY 1 MELOEYLHNEBEGDTYAKNAYNIALAKV-----KPELEOCIRELLRANIPNINKICV 56
DB 1 MKAYEVLHNNKNGGNGISTAYN---SLVORVILMKRPTTEQIDILVCSFPF---ETLCI 54
OY 57 ADGCGAGPNTLLVRDIYOSIDKVGQEKNELEPTIOIFLNDLFONDENVFKLLPSEF 116
DB 55 ADGCGAGPNTLLVRDIYOSIDKVGQEKNELEPTIOIFLNDLFONDENVFKLLPSEF 112
OY 117 YKLEKENGKRTIGSCLISAMPGFYGRLEPESMHFLSCYVHMLSOVPSGLVIELGIG 176
DB 113 QODLRQJGEEGPGFPGFSGVPSFYLRLPSSHLFHVSSYSLMMLSOVDP---LIE--- 166
OY 177 ANKGSYSSKCCRPVOKAYLDQFTKFTFLRIHSELFSRGMILLTICKVDEDEFN 236
DB 167 KKNENIYASTSPSPVAKAYKQEKDFSNFLKRSLELMKGKMYLTFGR---ESEDS 224
OY 237 P-----LDLDAINDLIVEGLLEEKLDSPNIPFTPSAEVKCIVEEGSCCLTYLE 290
DB 225 SKECCYIWEILLMLNLEVLGILEEKVDSPNIOYTPSPPEEKYIVREGSFTINRLE 284
OY 291 TKAHYDAAFSIDDDYVNSHEDIKAEY-VASLIRSYEPLASHGEAIMPDLFHLAK 349
DB 285 ATRVHNV-----SNEGINGVAVAKOMAAVEPLVSOFPDOKIMLVFOKYE 333
OY 350 HAAKVLHNGKGCYNLIISLAK 372
DB 334 IISDISEKTEFTINVIVLSLTK 356

RESULT 7
O9SRK6 PRELIMINARY; PRT; 392 AA.
AC 09SRK6:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE FLOAL NECTARY-SPECIFIC PROTEIN.
GN NTR1.
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20267007; PubMed-10809010;
RA Song J.T., Seo H.S., Song S.I., Lee J.S., Choi Y.D.;
RT "NMR encodes a floral nectary-specific gene in Brassica campestris L.
RT sp. pekinensis."
RL Plant Mol. Biol. 42:647-655(2000).
DR EMBL: AF179222; AAF22289.1;
SQ SEQUENCE 392 AA; 43815 MW; 25B78530E93B5757 CRC64;

Query Match 33.6%; Score 662.5; DB 10; Length 392;
Best Local Similarity 37.6%; Pred. No. 9.1e-49;
Matches 151; Conservative 77; Mismatches 131; Indels 43; Gaps 11;

```

```

OY 221 MLTLCICKVDEDEPNPL-----LDLDAINDLIVEGLLEEKLDSPNIPFTPSAE 272
DB 233 MVLSFGR-----SSDPPTTESCYOMELQALMSLAKGIIIEENIDAFNAPYLAASPE 288
OY 273 EVKCIYEESCEIILYEFRAHDAAFSIDDDYV---RSHEQIKAEYVASLIRSYEP 329
DB 289 ELMALTEKSSSIDRLSISYVDWEGSISDSDIYKFRPALASGRVAKTRAVAYEP 348
OY 330 ILSHGEAIMDLEHRLAKAAVLMKGCYNLIISLAK 371
DB 349 MLERTGQAVMDLEERTAKLVGEIVYSSPRITIVISLRL 390

RESULT 8
O9SPV4 PRELIMINARY; PRT; 359 AA.
AC 09SPV4:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE S-ADENOSYL-L-METHIONINE: SALICYLIC ACID CARBOXYL
DE METHYLTRANSFERASE.
GN SAMT.
OS Clarkia breweri.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Clarkia.
OX NCBI_TaxID=36903;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99306827; PubMed-10375393;
RA Ross J.R., Nam K.H., D'Auria J.C.;
RT "S-Adenosyl-L-methionine:salicylic acid carboxyl methyltransferase, an
RT enzyme involved in floral scent production and plant defense.
RT Arch. Biochem. Biophys. 367:9-16(1999).
RL Arch. Biochem. Biophys. 367:9-16(1999).
DR EMBL: AF133053; AAF00108.1;
SQ SEQUENCE 359 AA; 40289 MW; B0FE3E41ABBD851 CRC64;

Query Match 33.0%; Score 651.5; DB 10; Length 359;
Best Local Similarity 37.9%; Pred. No. 7.1e-48;
Matches 148; Conservative 75; Mismatches 119; Indels 49; Gaps 11;

```

```

RESULT 9
ID 09FY29 PRELIMINARY; PRT: 364 AA.
AC 09FY29
DT 01-MAR-2001 (TREMELREL, 16, Created)
DT 01-MAR-2001 (TREMELREL, 16, Last sequence update)
DT 01-JUN-2001 (TREMELREL, 17, Last annotation update)
DE SAM-BENZOIC ACID CARBOXYL METHYLTRANSFERASE.
GN BMT.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20312758; PubMed=10852939;
RA Dudareva N., Murfitt L.M., Mann C.J., Gorenstein N., Kolosova N.,
RA Kish C.M., Bonham C., Wood K.;
RT "Developmental Regulation of Methyl Benzoate Biosynthesis and Emission
RT in Snapdragon Flowers."
RT Plant Cell 12:949-961(2000).
RT EMBL: AF198492; AAF98284.1;
DR InterPro: IPR002106; AA.TRNA.LIGASE.11.
DR PROSITE: PS00339; AA.TRNA.LIGASE.11.2; UNKNOWN.1.
KW Transferase; Methyltransferase;
SQ SEQUENCE 364 AA; 41010 MW; C10C8E864A581419 CRC64;

Query Match 32.4%; Score 649.5; DB 10; Length 364;
Best Local Similarity 37.8%; Pred. No. 1.1e-47;
Matches 143; Conservative 85; Mismatches 122; Indels 31; Gaps 10;

QY 3 LQEVLMHN-EGEDDTSYAKNAS-YNLALAKVPELEQICRELLRANLPINIKCIKIVADLG 60
DB 4 MKKLCKMNGIDGDTSTANNSSGLOKYMMSKSLHYLDFTLKDIDGHV-GFPCCFMDMG 62
QY 61 CASGPNLTIVRDIOSIDKVGCEKNELEPRTIOIFLNDLFONDNSYFKLLPFYFKL 120
DB 63 CAGGNALTVASGIMTIEDL-YTEKININELPEFEVLNDLPNDENNFKL-----L 114
QY 121 EKENRRTGSGTISAMPGSYGRFLPPEESMHLSCSVMLHGOVSGVITELGANKG 180
DB 115 SHEN-----GNCFYVGLPGSFYGRFLPKSLHFAVSSYIMLSQVEGLE-----DNKRQ 165
QY 181 STYSSKGRPPVOKAYLDQFTTFLRISKELFSGRMULTICICKYDERDEPNPID- 239
DB 166 NTKMTESPPEVTKAKOTERDPSTFLKREELVPGGRVLFNGR--SVEDPSKDD 223
QY 240 -----LDMALINDIVLGELEEKLDSEFNIPPTPSAEVYKCIVEEGSCETIYETKA 294
DB 224 LAIFTLAKTLVMAEGVKKMDLYSFNIPYSPCTREVEAAILSEGSFTLDRLVFRV 283
QY 295 HYDAFSDIDD--YVPRSHQIKAEYVASLRSYEPTLASHGGAIMPDLFHLAKHA 351
DB 284 CNDASDYDDDDDDDDPSIFGKQSGFVADCVRAITEPMILASHGSGTINDLLFGYAKKI 343
QY 352 AKVLMGKGCNNLIISLAK 372
DB 344 VEHLSVENSYSFIVLSLR 364

RESULT 10
ID 09AR07 PRELIMINARY; PRT: 389 AA.
AC 09AR07
DT 01-JUN-2001 (TREMELREL, 17, Created)
DT 01-JUN-2001 (TREMELREL, 17, Last sequence update)
DT 01-JUN-2001 (TREMELREL, 17, Last annotation update)
DE S-ADENOSYL-L-METHIONINE:JASMONIC ACID CARBOXYL METHYLTRANSFERASE.
GN JMT.
OS Arabidopsis thaliana (Mouse-ear cress).

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11287667;
RA Seo H.S., Song J.T., Cheong J.J., Lee Y.H., Lee Y.W., Hwang I.,
RA Lee J.S., Choi Y.D.;
RT "Jasmonic acid carboxyl methyltransferase: A key enzyme for jasmonate-
RT regulated plant responses."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4788-4793(2001).
RX EMBL: AY008435; AAC23344.1;
DR EMBL: AY008434; AAC23343.1;
SQ SEQUENCE 389 AA; 43372 MW; 75A819E77662A18E CRC64;

Query Match 32.4%; Score 639; DB 10; Length 389;
Best Local Similarity 37.8%; Pred. No. 9.4e-47;
Matches 151; Conservative 79; Mismatches 129; Indels 40; Gaps 12;

QY 1 MELQEVLMHN-EGEDDTSYAKNASYNLALAKV-KPELEQICRELLRANLPINIKCIKIVADL 59
DB 1 MEVNRVLMHNGNGNETSYAKNSTAQSNIISLGRVMDALTKLMNSN--SEISSIGIDL 58
QY 60 GAGSAPNLTIVRDIOSIDKVGCEKNELEPRT--IOIFLNDLFONDNSYFKLLPFYFKL 117
DB 59 GCSGPNLSLISNIVDTINLCP-----DLDRPELVSLNDLPSPDFYICASLPFY 114
QY 118 RLKEKNGRKIG-----SCLISAMPGSFYGRFLPPEESMHLSCSVMLHGOVSGVITELGANKG 166
DB 115 --DRYNNKRELGFGRGCGECSVAGSFTGRFLPRSLHVAHSSSLHMLSVPCR 171
QY 167 -----SGVIELGIGANKSISYSGKCRPPVOKAYLDQFTKDTFTFLRISHKELFSGR 220
DB 172 EAEREDRTTAL--ENMGKITYISKTSRPSAKKAYALQFOTDVLVLRSESELVPGGR 228
QY 221 MLTCTICK--VDEFEDEPN--PLDLDMAINDIVLGELEEKLDSEFNIPPTPSAEVYK 276
DB 229 MYLSFGRSRSLDPTTEESCYOMELLAQALMSNAKEGIIIEEKIDAFNAPYAAASELKM 288
QY 277 IVEEGSCETIYETFKAHYDAFSDIDDV--YVPRSHQIKAEYVASLRSYEPTLASHGGA 332
DB 289 VIKKESSFDIDLEISPIDWEGSISESYDLAIRKPEALASGRVSNIRAVVEPMLE 348
QY 333 SHRGEAIMPDLFHLAKHAAYLMGKGCNNLIISLAK 371
DB 349 PTGENVMDLPERIAKIVGEYFVSSPRATVILSLVR 387

RESULT 11
ID 09LRLS PRELIMINARY; PRT: 368 AA.
AC 09LRLS
DT 01-OCT-2000 (TREMELREL, 15, Created)
DT 01-OCT-2000 (TREMELREL, 15, Last sequence update)
DT 01-DEC-2001 (TREMELREL, 19, Last annotation update)
DE S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE
DE PROTEIN. FLORAL NECTARY-SPECIFIC PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX SPRATN-COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;

```

Query Match	32.2%	Score 635.5	DB 10	Length 366
Best Local Similarity	38.0%	Pred. No. 1.8e-46		
Matches 148	Conservative 74	Mismatches 122	Indels 45	Gaps
Query	6	VLAHNEGGDTSYARNASNYLAL-AKVKFLFECQIRRELL-RANLPNINKCIKADGACAS	63	
Db	3	VSMKGGDESVYANNSEDAOKSITSDAKPEKMSVEMIVKMDPPG---CIKADGACSS	59	
Query	64	GPMPLLVADIVQISIDKVGQEKNELEPPIOLFINDIFONDPSVKRLPSRYRLEKE	123	
Db	60	GEMTFVLWSEIVTITITTYQONGNL--PEIDOCINDLPENDFTFKLPSRHEKL-KM	116	
Query	124	NGRRICSCISAMPSFGRFPRESMHFLSCSYVHMLSOVPGCLVIELGANKGSIY	183	
Db	117	NVK--GNCVSCPCSPSTFLTRPEKSLHETHYSFCLHMLSKVPGCL-----ENKNKVIY	168	
Query	184	SSGCGPPQAKYLDQFQKDTTFLRAHSEKLEFSGRMLTCTCK--VDEPDEP--NPDL	239	
Db	169	LRSFPPNLYESTINQFKDQSMFLRRRADETPSGRMALTLVARKLIDPLSKECKDMS	228	
Query	240	LIDMAINDLIVELGEELEEKLDSEFNIPETPSAEVKACVIEEGSCCELLYET-----F	292	
Db	229	LVSDDLIVDSVGGVKKEDSEFNLPLVSPDSSEVKEVIEENGSEFEKNEETFGILLTSY	288	
Query	293	KARYDAFSDIDDPV-VSHSQIKAEVYASLIRSYEPFLVLSHNGEAIMPDLEHRLAKHA	351	
Db	289	KTHSEVKKDDDDVDHDSRREYVKTR--ANMRSIIEPMVAHNGEALIDRLDKYIYHA	346	
Query	352	AKYLHMGKGCYN-----NLIIISLAKK	372	
Db	347	CQ-----RYDTLRNKPTYNFVSLTRK	368	

RESULT 12

09FJ26

09FJ26 PRELIMINARY: PRT: 354 AA.

AC 09FJ26:

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE 5-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL METHYLTRANSFERASE-LIKE PROTEIN.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OC NOBI\_Taxid-3702;

OX [1]

RA RA

RA REBANI H., NAKAMURA Y., SATO S., ASAMIZU E., KANEKO T., MIYAJIMA N.,

RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.

RT Sequence features of the regions of 1,367,185 bp covered by 19

RT DNA Res. 5:203-216(1998)."

DR EMBL; AB013389; BAB10319.1; -

DR TRANSFAC; Methyltransferase.

KW SEQUENCE 366 AA; 4201 MW; 119D369E8A1B14B6 CRC64;

Query Match 32.1%; Score 633; DB 10; Length 354;  
Best Local Similarity 39.6%; Pred. No. 2,76-46;  
Matches 151; Conservative 63; Mismatches 123; Indels 44; Gaps 12

QY 9 MNEGEDTGYANA--SYNLATAKYKPTLDGCR-ELBANIPINNKIKYADGASGPN 66  
DB 1 MSGGDGNSYTSNLSLOKKYAKSKPKPLVANKTGKMINLPNT---TKVADGCGTGEN 57  
QY 67 TLTAVDIYOSIDKVGQEKNEKLERPTIQIPLNDLFONDENVSKLLPSFYRLEKENG 126  
DB 58 TLTAVMEIYNTVNLVLCQOCNO--KPEPIDCLNDLPDNDFTFKFPEFNKVKSKR-- 113  
QY 127 KIGSCGISAPGSFYGRLEFPESNMFLHSCSYNHLMSOVPGELIYELGIGANKGSIVSSK 186  
DB 114 ---LCYVSPGSPFSYRLEFPKSLHEFHSYSSILHMLSKYKGL-----EKNSSVYITT 164  
QY 187 GCRPVQKAVLDQFPKDPFTPLRHSKELTFSGKRLCLTCIKVDEPDEPND-----L 240  
DB 165 SSPPNAYKAVLWQFSDPKSFLEMRSESNVNGRYVLTFLIR-KTDDPLHRDCHFWTL 223  
QY 241 LDMAINDIVELLLEELKLSFNIPFTTSAEVYCYIEEGSCGLIYLETFRANYDAF 300  
DB 224 LSTSLRGLYELVSKASVDSFNPLFSDSKKEVEMKRNKGSEIYNDLEIR-----GF 277  
QY 301 SI-----DDYFVRSHEQIKAEYVALIRSVEYPTLASHFGEALIMPLERHAKRAAVL 355  
DB 278 ELGISHHDDYVLLHQSIAKQAFRANCIRAVSEMLVADFGVDMITDLTKFKAHYVSO-- 335  
QY 356 HMGKGCYN---NLIIISLAKK 372  
DB 336 --HASCNTKTYTLVAVSLIRK 354

RESULT 13  
ID 09LS20  
ID 09LS20 PRELIMINARY: PRT: 363 AA.  
AC 09LS20:  
DI 01-OCT-2000 (TREMBLrel. 15, Created)  
DI 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DI 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DI S-ADENOSYL-L-METHIONINE:SALICYLIC ACID CARBOXYL  
DI METHYLTRANSFERASE-LIKE  
DI Arabidopsis thaliana (Mouse-ear cress).  
DI Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
DI OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
DI OC eucrods II; Brassicales; Brassicaceae; Arabidopsis.  
DI NCBI\_Taxid-3702;  
DI 11  
DI SEQUENCE FROM N. A.  
DI SPRAIN-COLUMBIA;  
DI Kaneko T., Katoh T., Asanuma E., Sato S., Nakamura Y., Kotani H.,  
DI Tadea S.;  
DI Structural analysis of Arabidopsis thaliana chromosome 5. XI.";  
DI Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DI EMBL: AB028606; BAA97354.1;  
DI InterPro: IPR000794; Kctac1-synt.  
DI PROSITE: P500606; B\_KETOACYL\_SYNTHASE; UNKNOWN\_1;  
DI SEQUENCE 363 AA; 41154 MW; 4C6161A0B4B34108 CRC64;

Query Match 31.9%; Score 629; DB 10; Length 363;  
Best Local Similarity 39.5%; Pred. No. 6,2e-46;  
Matches 146; Conservative 61; Mismatches 111; Indels 52; Gaps 12

QY 9 MNGEGDTSYKNSNYMLAL-KRPELEOCIRELT-RANLPINMCIVADIGASGPN 66  
DB 1 MKGSDGHSYANNEGOKRIASAKRYVEYIKVKTDPG---CLVADLGCGSEN 57  
QY 67 TLTAVDIYOSIDKVGQEKNEKLERPTIQIPLNDLFONDENVSKLLPSFYRLEKENG 126  
DB 58 TLTAVMEIYNTVNLVLCQOCNO--KPEPIDCLNDLPDNDFTFKFPEFNKVKSKR-- 113  
QY 127 KIGSCGISAPGSFYGRLEFPESNMFLHSCSYNHLMSOVPGELIYELGIGANKGSIVSSK 186  
DB 114 ---LCYVSPGSPFSYRLEFPKSLHEFHSYSSILHMLSKYKGL-----EKNSSVYITT 164  
QY 187 GCRPVQKAVLDQFPKDPFTPLRHSKELTFSGKRLCLTCIKVDEPDEPND-----L 240  
DB 165 SSPPNAYKAVLWQFSDPKSFLEMRSESNVNGRYVLTFLIR-KTDDPLHRDCHFWTL 223  
QY 241 LDMAINDIVELLLEELKLSFNIPFTTSAEVYCYIEEGSCGLIYLETFRANYDAF 300  
DB 224 LSTSLRGLYELVSKASVDSFNPLFSDSKKEVEMKRNKGSEIYNDLEIR-----GF 277  
QY 301 SI-----DDYFVRSHEQIKAEYVALIRSVEYPTLASHFGEALIMPLERHAKRAAVL 355  
DB 278 ELGISHHDDYVLLHQSIAKQAFRANCIRAVSEMLVADFGVDMITDLTKFKAHYVSO-- 335  
QY 356 HMGKGCYN---NLIIISLAKK 372  
DB 336 --HASCNTKTYTLVAVSLIRK 354

```

QY 127 KISSCLISAMPSFGYGRFPRESMHFHSYVHWSOVPSGLVIELGIGANKSIYSSK 186
DB 113 VKKCKISVPSGFSRFLPSKSLHFSHSLCLHWSKYPDGL-----EDNKKNYLNS 166
QY 187 GCBPPOKAYLDQFTKDTTFLRIHSKEFLSRGMMLTICICVDEFPDPLDLDN--- 243
DB 167 PCBPVYKSYLQFKNPDSLEFLRADELYPNKRMALFVGR-----KSLDPLSDCP 219
QY 244 -----AINDIYEGLEEEKLDSFNIFPFPSSAEKYCIVEEGSCGELILEYFKRH 295
DB 220 QMSSISDLDLVSEGVKSDVDNSNLFIFPDESEVREYIESEGSKISNFEIT--- 276
QY 296 YDAAFSI-----DDDYVRSHEDIKAEVY--ASLRSVYEPILASHFGGALMPDL 343
DB 277 FGLLEFYKTKRGTEVYKDDDD---NLDOSCFEYIKRRASTINSITEPMIGHFGDALMDRL 333
QY 344 FHLRAKHAH 353
DB 334 FERYTHLAE 343

```

```

RESULT 14
ID 09FZNR PRELIMINARY; PRT: 369 AA.
AC 09FZNR;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CAFFEINE SYNTHASE.
GN TCS1.
OS Camellia sinensis (Tea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Theaceae; Camellia.
OX NCBI_TaxID=4442;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20437355; PubMed=10984041;
RA Kato M., Mizuno K., Crozier A., Fujimura T., Ashihara H.;
RL "Caffeine synthase gene from tea leaves.";
RL Nature 406:556-557(2000).
RL EMBL; AB031280; BAB12278.1;
SQ SEQUENCE 369 AA; 41272 MW; E6D262087E475576 CRC64;

```

```

Query Match 31.8%; Score 628; DB 10; Length 369;
Best Local Similarity 36.3%; Pred. No. 7.8e-46;
Matches 143; Conservative 80; Mismatches 113; Indels 56; Gaps 11;
QY 2 ELQEVLMHNGEGSDTSYAKNASYNLAKV KPLFEOCIRELLRANLPINCKIRVADLG 60
DB 8 KNYEVLPMHNGEGSDTSYAKNASYNLAKV KPLFEOCIRELLRANLPINCKIRVADLG 60
QY 61 CASGPNLTLLVADIVOSIDKVGQEEKNELERPT--IQIFLNDLFQNDFNSVFLLPSFYRL 118
DB 66 CASGPNLTLLVADIVOSIDKVGQEEKNELERPT--IQIFLNDLFQNDFNSVFLLPSFYRL 118
QY 119 KLEKENGKTKS-----CLISAMPSFGYGRFPRESMHFHSYVHWSOVPSGLVIE 172
DB 119 EVINCKKEEPPCYVMGVPSFSGHRLFPNNSHLHLSYVHWSOVPSGLVIE 172
QY 173 LGIGANKSIYSSKGRFPPOKAYLDQFTKDTTFLRIHSKEFLSRGMMLTICICVDE 232
DB 172 EGIANKRKIIISTSPYVKEKLSQFHEDTFLMARSQEVNPGCMVL--ILNGRC 229
QY 233 DEPNL-----DLIDMAINDLIVEGLEEEKLDSFNIPFPSSAEVYKIVEEGSCGELI 286
DB 230 SPSPSMOCGFWELLMALMAYLSQGLIDEDKLDIFNIPSPASLEVKQIVRDSGFTI 289
QY 287 LYLEFKRHAYAAFSIDDPVYRSHEDIKAEVYASLRSVYEPILASHFGGALMPDLFHR 346
DB 290 DHLE-----GFDLDSVEMQENDKRWNGEFTKYVNAFTFELISNQSPFELIMKLDK 341

```

```

QY 347 LAKHAAVLMHGKGCYNMLIIS--LAKKPEKSDV 378
DB 342 -----FTHIVSDLEAKILPKTTSI 360
RESULT 15
ID 023234 PRELIMINARY; PRT: 371 AA.
AC 023234;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHEICAL 42.0 KDA PROTEIN.
GN C7A10.890 OR A74G36470.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Terry N., Vos P., Heljnen L., Mewes H.W., Schueller C.,
RA Chaitwalz N.,
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; Z59708; CAB16845.1;
RL EMBL; AL161589; CAB80313.1;
RL Hypothetical protein.
SQ SEQUENCE 371 AA; 41984 MW; F5EB391E83CB6A90 CRC64;

```

```

Query Match 31.2%; Score 614.5; DB 10; Length 371;
Best Local Similarity 39.5%; Pred. No. 1.1e-44;
Matches 139; Conservative 64; Mismatches 126; Indels 23; Gaps 8;
QY 2 ELQEVLMHNGEGSDTSYAKNASYNLAKV KPLFEOCIRELLRANLPINCKIRVADLG 60
DB 5 DMEREFMTGGDGKTSYAKNASYNLAKV KPLFEOCIRELLRANLPINCKIRVADLG 60
QY 61 CASGPNLTLLVADIVOSIDKVGQEEKNELERPT--IQIFLNDLFQNDFNSVFLLPSFYRL 120
DB 62 CASGPNLTLLVADIVOSIDKVGQEEKNELERPT--IQIFLNDLFQNDFNSVFLLPSFYRL 120
QY 121 EKENGKTKS-----CLISAMPSFGYGRFPRESMHFHSYVHWSOVPSGLVIELGIGA 177
DB 122 KRDNVN--GPCBVFVFLAAYPSPFGYGRFPRESMHFHSYVHWSOVPSGLVIELGIGA 177
QY 178 NKGSYSSKGRFPPOKAYLDQFTKDTTFLRIHSKEFLSRGMMLTICIC--VDERDEP 235
DB 180 NKGSYSSKGRFPPOKAYLDQFTKDTTFLRIHSKEFLSRGMMLTICIC--VDERDEP 235
QY 236 NPL--DLIDMAINDLIVEGLEEEKLDSFNIPFPSSAEVYKIVEEGSCGELILEYFKR 293
DB 240 NSFPEWELLSSTADIYVAGETEEERKLDSDYMHFYASADEIGEDVKGSGSELEERLEME 299
QY 294 AYDAAFSIDD-DYVRSHEDIKAEVYASLRSVYEPILASHFGGALMPDLF 344
DB 300 VKDKNGTEGDISY-----GKAAVAKTVRAVQESMLVQHFGKILDKLF 342

```

Search completed: July 27, 2002, 05:42:16  
Job time: 492 sec

---